

#5

SEQUENCE LISTING

Garman, Jonathan David
Candia III, Albert Frederick
Arbor Vita Corporation

<120> CLASP-3 Transmembrane Protein

<130> 020054-000311US

<140> US 09/737,246

<141> 2000-12-13

<150> US 60/160,860

<151> 1999-10-21

<150> US 60/162,498

<151> 1999-10-29

<150> US 60/170,453

<151> 1999-12-13

<150> US 60/176,195

<151> 2000-01-14

<150> US 60/182,296

<151> 2000-02-14

<150> US 09/547,276

<151> 2000-04-11

<150> US 60/196,267

<151> 2000-04-11

<150> US 60/196,460

<151> 2000-04-11

<150> US 60/196,527

<151> 2000-04-11

<150> US 60/196,528

<151> 2000-04-11

<150> US 09/687,837

<151> 2000-10-13

<150> US 60/240,503

<151> 2000-10-13

<150> US 60/240,508

<151> 2000-10-13

<150> US 60/240,539

<151> 2000-10-13

<150> US 60/240,543

<151> 2000-10-13

<160> 148

<170> PatentIn Ver. 2.1

<210> 1

<211> 6828

<212> DNA

<213> Homo sapiens

<220>

<223> full-length human CLASP-3 cDNA

<220>

<221> CDS

<222> (22)..(6294)

<223> human CLASP-3

<400> 1

gtcgccgtcg ccgcagcagc c atg gcc gag cgc cgc gcc ttc gcc cag aag	51
Met Ala Glu Arg Arg Ala Phe Ala Gln Lys	
1 5 10	

atc agc aga acg gtg gca gcc gaa gtt agg aag cag atc tcc gga caa	99
Ile Ser Arg Thr Val Ala Ala Glu Val Arg Lys Gln Ile Ser Gly Gln	
15 20 25	

tat agt ggt tct ccc caa ctg ctc aaa aac ctt aat att gtt ggc aat	147
Tyr Ser Gly Ser Pro Gln Leu Leu Lys Asn Leu Asn Ile Val Gly Asn	
30 35 40	

ata tcc cat cac acc aca gtg ccc ctt acc gaa gca gta gat cca gtg	195
Ile Ser His His Thr Thr Val Pro Leu Thr Glu Ala Val Asp Pro Val	
45 50 55	

gat ttg gaa gat tac ctc att act cat cct ttg gct gtg gat tct ggg	243
Asp Leu Glu Asp Tyr Leu Ile Thr His Pro Leu Ala Val Asp Ser Gly	
60 65 70	

cct tta cgg gat ttg att gaa ttt cct cca gat gat att gaa gtt gtt	291
Pro Leu Arg Asp Leu Ile Glu Phe Pro Pro Asp Asp Ile Glu Val Val	
75 80 85 90	

tat agt cct cgg gac tgc aga act ctt gtt tca gct gta cct gaa gaa	339
Tyr Ser Pro Arg Asp Cys Arg Thr Leu Val Ser Ala Val Pro Glu Glu	
95 100 105	

agt gaa atg gat cca cat gtt aga gac tgt ata aga agt tat aca gaa	387
Ser Glu Met Asp Pro His Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu	
110 115 120	

gac tgg gca att gtc atc aga aaa tat cat aaa ttg gga aca gga ttt	435
Asp Trp Ala Ile Val Ile Arg Lys Tyr His Lys Leu Gly Thr Gly Phe	
125 130 135	

aat ccc aat aca tta gat aaa cag aaa gaa agg caa aaa ggt ttg cca	483
Asn Pro Asn Thr Leu Asp Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro	
140 145 150	

aaa caa gtt ttt gaa tct gat gaa gct cca gat ggc aac agc tac cag	531
Lys Gln Val Phe Glu Ser Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln	
155 160 165 170	

gat	gat	caa	gat	gac	ctt	aaa	aga	cgt	tca	atg	tca	ata	gat	gat	acc	579
Asp	Asp	Gln	Asp	Asp	Leu	Lys	Arg	Arg	Ser	Met	Ser	Ile	Asp	Asp	Thr	
																175
																180
																185
cca	agg	ggt	agc	tgg	gcc	tgt	agt	atc	ttt	gac	ttg	aaa	aat	tca	ctt	627
Pro	Arg	Gly	Ser	Trp	Ala	Cys	Ser	Ile	Phe	Asp	Leu	Lys	Asn	Ser	Leu	
																190
																195
																200
cct	gat	gct	ttg	ctt	ccc	aat	tta	ctt	gat	cga	act	cca	aat	gaa	gaa	675
Pro	Asp	Ala	Leu	Leu	Pro	Asn	Leu	Leu	Asp	Arg	Thr	Pro	Asn	Glu	Glu	
																205
																210
																215
ata	gac	cgt	cag	aat	gat	gac	caa	agg	aaa	tca	aac	cgt	cac	aaa	gaa	723
Ile	Asp	Arg	Gln	Asn	Asp	Asp	Gln	Arg	Lys	Ser	Asn	Arg	His	Lys	Glu	
																220
																225
																230
ctt	ttt	gct	ttg	cat	cca	tca	cca	gat	gag	gaa	gaa	cca	ata	gaa	cgg	771
Leu	Phe	Ala	Leu	His	Pro	Ser	Pro	Asp	Glu	Glu	Glu	Pro	Ile	Glu	Arg	
																235
																240
																245
																250
ctt	agt	gtt	cct	gat	ata	ccc	aaa	gaa	cat	ttt	ggt	caa	aga	ctt	ctt	819
Leu	Ser	Val	Pro	Asp	Ile	Pro	Lys	Glu	His	Phe	Gly	Gln	Arg	Leu	Leu	
																255
																260
																265
gta	aaa	tgc	tta	tca	ctc	aag	ttt	gaa	att	gaa	att	gaa	ccc	att	ttt	867
Val	Lys	Cys	Leu	Ser	Leu	Lys	Phe	Glu	Ile	Glu	Ile	Glu	Pro	Ile	Phe	
																270
																275
																280
gca	agt	ttg	gct	tta	tat	gat	gtc	aag	gaa	aag	aaa	aag	att	tca	gaa	915
Ala	Ser	Leu	Ala	Leu	Tyr	Asp	Val	Lys	Glu	Lys	Lys	Lys	Ile	Ser	Glu	
																285
																290
																295
aac	ttt	tat	ttt	gac	ctt	aat	tct	gag	cag	atg	aaa	ggg	ttg	tta	cgt	963
Asn	Phe	Tyr	Phe	Asp	Leu	Asn	Ser	Glu	Gln	Met	Lys	Gly	Leu	Leu	Arg	
																300
																305
																310
cca	cat	gta	cca	cct	gct	gcc	att	act	acc	ctg	gca	aga	tca	gca	att	1011
Pro	His	Val	Pro	Pro	Ala	Ala	Ile	Thr	Thr	Leu	Ala	Arg	Ser	Ala	Ile	
																315
																320
																325
																330
ttt	tct	atc	act	tat	cct	tcc	caa	gat	gtt	ttt	ctt	gta	ata	aag	cta	1059
Phe	Ser	Ile	Thr	Tyr	Pro	Ser	Gln	Asp	Val	Phe	Leu	Val	Ile	Lys	Leu	
																335
																340
																345
gaa	aaa	gtc	cta	cag	caa	gga	gac	att	gga	gag	tgt	gca	gaa	cca	tat	1107
Glu	Lys	Val	Leu	Gln	Gln	Gly	Asp	Ile	Gly	Glu	Cys	Ala	Glu	Pro	Tyr	
																350
																355
																360
atg	att	ttc	aaa	gaa	gca	gat	gcc	acc	aag	aat	aaa	gaa	aaa	ctg	gag	1155
Met	Ile	Phe	Lys	Glu	Ala	Asp	Ala	Thr	Lys	Asn	Lys	Glu	Lys	Leu	Glu	
																365
																370
																375
aaa	ctg	aag	agt	caa	gca	gat	cag	ttt	tgc	caa	aga	ctt	ggg	aaa	tat	1203
Lys	Leu	Lys	Ser	Gln	Ala	Asp	Gln	Phe	Cys	Gln	Arg	Leu	Gly	Lys	Tyr	
																380
																385
																390
cgc	atg	cct	ttt	gct	tgg	act	gca	atc	cat	tta	atg	aat	att	gtt	agc	1251
Arg	Met	Pro	Phe	Ala	Trp	Thr	Ala	Ile	His	Leu	Met	Asn	Ile	Val	Ser	
																395
																400
																405
																410

agt gct ggg agt ttg gaa aga gat tct aca gaa gta gaa atc agt act		1299
Ser Ala Gly Ser Leu Glu Arg Asp Ser Thr Glu Val Glu Ile Ser Thr		
415	420	425
gga gaa cga aaa ggg tct tgg tca gag agg agg aat tct agt att gtt		1347
Gly Glu Arg Lys Gly Ser Trp Ser Glu Arg Arg Asn Ser Ser Ile Val		
430	435	440
ggc aga cga tca ctt gaa agg aca aca agt gga gat gat gct tgt aac		1395
Gly Arg Arg Ser Leu Glu Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn		
445	450	455
ttg acg agc ttt cga cca gct act ctc aca gtg aca aat ttt ttt aag		1443
Leu Thr Ser Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys		
460	465	470
cag gaa gga gac cgc tta agt gat gaa gat ctc tac aaa ttc ctt gct		1491
Gln Glu Gly Asp Arg Leu Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala		
475	480	490
gat atg aga agg cca tct tct gtc tta cg ^g cga cta aga cct att aca		1539
Asp Met Arg Arg Pro Ser Ser Val Leu Arg Arg Leu Arg Pro Ile Thr		
495	500	505
gct cag ctc aag ata gac att tct ccc gca cct gaa aat ccc cat tat		1587
Ala Gln Leu Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Tyr		
510	515	520
tgc cta act ccg gag ctg ctt caa gtg aag ctt tac cct gac agt aga		1635
Cys Leu Thr Pro Glu Leu Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg		
525	530	535
gtt aga cct acc aga gaa atc tta gag ttt ccc gca agg gat gtt tat		1683
Val Arg Pro Thr Arg Glu Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr		
540	545	550
gtt cca aac act act tac aga aat ctt ctc tac ata tac cct cag agt		1731
Val Pro Asn Thr Thr Tyr Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser		
555	560	565
570		
ctt aat ttt gcc aat cgt caa ggt tct gct aga aat ata aca gtg aaa		1779
Leu Asn Phe Ala Asn Arg Gln Gly Ser Ala Arg Asn Ile Thr Val Lys		
575	580	585
gtc cag ttt atg tat gga gag gat cca agc aat gcc atg ccg gta atc		1827
Val Gln Phe Met Tyr Gly Glu Asp Pro Ser Asn Ala Met Pro Val Ile		
590	595	600
ttt ggt aaa tct agc tgt tca gaa ttt tca aag gaa gcc tat aca gcc		1875
Phe Gly Lys Ser Ser Cys Ser Glu Phe Ser Lys Glu Ala Tyr Thr Ala		
605	610	615
gta gta tat cat aac agg tct cct gat ttt cat gaa gaa atc aag gtt		1923
Val Val Tyr His Asn Arg Ser Pro Asp Phe His Glu Glu Ile Lys Val		
620	625	630
aag ctt cct gct act tta act gac cat cat cac ttg ctt ttt act ttt		1971
Lys Leu Pro Ala Thr Leu Thr Asp His His His Leu Leu Phe Thr Phe		
635	640	645
		650

tat cat gtt agt tgt caa caa aaa caa aat act cct ctt gaa aca cca		2019	
Tyr His Val Ser Cys Gln Gln Lys Gln Asn Thr Pro Leu Glu Thr Pro			
655	660	665	
gtt gga tat aca tgg ata cca atg ctt cag aat gga cggttg aag act		2067	
Val Gly Tyr Thr Trp Ile Pro Met Leu Gln Asn Gly Arg Leu Lys Thr			
670	675	680	
ggc cag ttt tgc ttg cca gtc tca ttg gaa aaa cca cca cag gct tat		2115	
Gly Gln Phe Cys Leu Pro Val Ser Leu Glu Lys Pro Pro Gln Ala Tyr			
685	690	695	
tct gta ctg tct cct gag gtt cct cta cct ggc atg aaa tgg gta gat		2163	
Ser Val Leu Ser Pro Glu Val Pro Leu Pro Gly Met Lys Trp Val Asp			
700	705	710	
aat cac aaa ggt gtt ttt aat gtt gaa gtt gtt gct gtt tcgtct atc		2211	
Asn His Lys Gly Val Phe Asn Val Glu Val Val Ala Val Ser Ser Ile			
715	720	725	730
cat aca caa gat cct tat ctt gac aaa ttt ttt gct ctg gtc aat gct		2259	
His Thr Gln Asp Pro Tyr Leu Asp Lys Phe Phe Ala Leu Val Asn Ala			
735	740	745	
ctg gat gaa cac ctg ttc cca gtc cga att ggg gac atg cga atc atg		2307	
Leu Asp Glu His Leu Phe Pro Val Arg Ile Gly Asp Met Arg Ile Met			
750	755	760	
gaa aat aac tta gaa aat gaa ttg aag agc agt att tca gca ctg aat		2355	
Glu Asn Asn Leu Glu Asn Glu Leu Lys Ser Ser Ile Ser Ala Leu Asn			
765	770	775	
tca tcc cag ctg gaa cca gtg gtc cga ttt ctt cat ctt ctg cta gat		2403	
Ser Ser Gln Leu Glu Pro Val Val Arg Phe Leu His Leu Leu Leu Asp			
780	785	790	
aaa ctg ata ctt tta gtt att aga cct cct gtc att gct ggc caa ata		2451	
Lys Leu Ile Leu Leu Val Ile Arg Pro Pro Val Ile Ala Gly Gln Ile			
795	800	805	810
gtt aac cta ggt caa gca tct ttt gaa gcc atg gca tca att ata aat		2499	
Val Asn Leu Gly Gln Ala Ser Phe Glu Ala Met Ala Ser Ile Ile Asn			
815	820	825	
cga ctt cac aaa aac ttg gaa gga aat cat gac cag cat ggc aga aac		2547	
Arg Leu His Lys Asn Leu Glu Gly Asn His Asp Gln His Gly Arg Asn			
830	835	840	
agc ctt ctt gca tca tat att cat tat gtt ttc cgc cta cca aat act		2595	
Ser Leu Leu Ala Ser Tyr Ile His Tyr Val Phe Arg Leu Pro Asn Thr			
845	850	855	
tac cct aat tca tca tca cca ggt cct ggg ggt ttg gga gga tca gtg		2643	
Tyr Pro Asn Ser Ser Pro Gly Pro Gly Gly Leu Gly Gly Ser Val			
860	865	870	
cat tat gcc aca atg gct aga tct gcg gtg aga cct gca agc ctt aat		2691	
His Tyr Ala Thr Met Ala Arg Ser Ala Val Arg Pro Ala Ser Leu Asn			
875	880	885	890

tta aat cgt tct cga agc ctt agt aat agc aat cca gat ata tct ggg Leu Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly	2739
895 900 905	
act ccc acg tca cca gat gat gaa gtt cga tca atc atc ggg agt aag Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile Gly Ser Lys	2787
910 915 920	
ggt tta gat cgc tcc aat tcc tgg gtt aac act ggt ggt cca aaa gct Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly Pro Lys Ala	2835
925 930 935	
gcc cca tgg gga tcc aac ccc agt cca agt gca gaa tca aca cag gct Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala	2883
940 945 950	
atg gat cga agt tgt aat cgt atg tct tcg cac aca gag acg tca agt Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu Thr Ser Ser	2931
955 960 965 970	
ttc tta caa aca tta acg gga cgc tta cca act aaa aag ctt ttt cac Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys Leu Phe His	2979
975 980 985	
gag gag ctg gct ttg cag tgg gtt gtt tgc agt ggc agc gtt cgaa gaa Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser Val Arg Glu	3027
990 995 1000	
tca gct ttg caa caa gcc tgg ttc ttt ttt gaa tta atg gta aag agc Ser Ala Leu Gln Gln Ala Trp Phe Phe Glu Leu Met Val Lys Ser	3075
1005 1010 1015	
atg gtg cac cat tta tac ttt aat gat aaa ctt gag gct cca agg aaa Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys	3123
1020 1025 1030	
agt cgt ttt cca gaa cgt ttc atg gat gac att gca gct ctt gtc agc Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala Leu Val Ser	3171
1035 1040 1045 1050	
acg att gct agt gat ata gtt tca cga ttt cag aag gac aca gaa atg Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp Thr Glu Met	3219
1055 1060 1065	
gtt gag aga ctc aat aca agc ctt gca ttc ttt ctc aat gat ctg ttg Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu	3267
1070 1075 1080	
tct gtt atg gac aga gga ttt gtt ttt agc ctt ata aag tcc tgc tat Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr	3315
1085 1090 1095	
aaa cag gtg tct tca aag ctt tac tca tta ccg aat ccc agt gtt ctg Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu	3363
1100 1105 1110	
gtg tcc ttg agg ctg gat ttt cta cga atc atc tgc agt cat gag cac Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser His Glu His	3411
1115 1120 1125 1130	

tat gtt aca tta aac tta ccc tgc agc tta ctt act cca cct gca tct			3459
Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser			
1135	1140	1145	
cca tca cct tct gtt tct tct gca aca tct cag agt tct gga ttt tct			3507
Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser			
1150	1155	1160	
acg aat gta caa gac caa aag att gca aat atg ttt gaa tta tcc gtg			3555
Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu Leu Ser Val			
1165	1170	1175	
cct ttc cgc caa cag cat tat ttg gca gga ctt gtg tta aca gag ctg			3603
Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu			
1180	1185	1190	
gct gtc att tta gac cct gat gct gaa gga ctg ttt gga ttg cat aag			3651
Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly Leu His Lys			
1195	1200	1205	1210
aaa gtc atc aat atg gta cac aat tta ctc tcc agt cac gac tca gac			3699
Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His Asp Ser Asp			
1215	1220	1225	
ccg cgg tac tct gac cct cag ata aag gct cga gtg gcc atg ttg tat			3747
Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala Met Leu Tyr			
1230	1235	1240	
cta cct ctg att ggt att atc atg gaa act gta cct cag ctg tat gat			3795
Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln Leu Tyr Asp			
1245	1250	1255	
ttt aca gaa act cac aat caa cga gga aga cca att tgt ata gcc act			3843
Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr			
1260	1265	1270	
gat gat tat gaa agt gag agc gga agt atg ata agc cag acc gtt gcc			3891
Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln Thr Val Ala			
1275	1280	1285	1290
atg gca atc gca ggg aca tcg gtc cct caa cta aca agg cct ggc agt			3939
Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg Pro Gly Ser			
1295	1300	1305	
tcc ctc ctc acg tca acg agt ggc agg caa cac act acc ttt tca gca			3987
Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr Phe Ser Ala			
1310	1315	1320	
gaa tca agt cga agc ctt ttg atc tgt cta ctt tgg gtt ctc aaa aat			4035
Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val Leu Lys Asn			
1325	1330	1335	
gca gat gaa aca gtt cta cag aag tgg ttt aca gat ctc tca gtc ttg			4083
Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu Ser Val Leu			
1340	1345	1350	
cag cta aac cgg cta tta gat ctg ctt tat ctc tgt gtg tct tgc ttt			4131
Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe			
1355	1360	1365	1370

gag tat aaa ggg aaa aaa gtg ttt gaa cga atg aat agc ttg acc ttt			4179
Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser Leu Thr Phe			
1375	1380	1385	
aag aaa tca aaa gac atg aga gca aag ctt gaa gaa gct att ctt ggg			4227
Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly			
1390	1395	1400	
agc ata ggt gcc agg caa gaa atg gta cg ^g cga agc cga gga cag ctc			4275
Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg Gly Gln Leu			
1405	1410	1415	
gag aga agc cca tct gga agt gcc ttt gga agt caa gaa aat ttg agg			4323
Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg			
1420	1425	1430	
tgg agg aaa gat atg act cac tgg cgt caa aac aca gag aag ctt gac			4371
Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu Lys Leu Asp			
1435	1440	1445	1450
aaa tca aga gca gag att gaa cac gaa gca ctg att gat gga aac ctg			4419
Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp Gly Asn Leu			
1455	1460	1465	
gct aca gaa gca aac cta atc att tta gat aca tta gag att gtt gtt			4467
Ala Thr Glu Ala Asn Leu Ile Leu Asp Thr Leu Glu Ile Val Val			
1470	1475	1480	
cag acc gtt tct gta acg gaa tcc aaa gag agc att ctt ggt gga gtg			4515
Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu Gly Gly Val			
1485	1490	1495	
cta aaa gtg cta cta cac agc atg gcc tgt aac caa agt gca gtt tat			4563
Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser Ala Val Tyr			
1500	1505	1510	
cta caa cac tgt ttt gct aca cag aga gcc ttg gtt tca aag ttt cct			4611
Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser Lys Phe Pro			
1515	1520	1525	1530
gaa ctc tta ttt gaa gaa gag aca gag cag tgt gct gat tta tgc ctc			4659
Glu Leu Leu Phe Glu Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu			
1535	1540	1545	
agg ctt ctc cga cac tgt agc agt agc atc ggt aca ata cgg tca cac			4707
Arg Leu Leu Arg His Cys Ser Ser Ile Gly Thr Ile Arg Ser His			
1550	1555	1560	
ccc agt gcc tcc ctt tac cta atg agg caa aac ttt gag att ggg			4755
Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile Gly			
1565	1570	1575	
aat aac ttt gcc agg gtt aaa atg cag gta cca atg tca cta tcc tcc			4803
Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser Leu Ser Ser			
1580	1585	1590	
ttg gtg ggc aca tct cag aat ttt aat gaa gaa ttc tta aga cgt tct			4851
Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser			
1595	1600	1605	1610

cta aag act ata ttg aca tat gct gaa gaa gat ctg gaa ttg agg gaa			4899
Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu			
1615	1620	1625	
aca aca ttt cct gat cag gtc cag gat ctg gtt ttc aat ctc cat atg			4947
Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn Leu His Met			
1630	1635	1640	
att ctt tct gat act gtg aaa atg aag gaa cac cag gag gat cct gaa			4995
Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu Asp Pro Glu			
1645	1650	1655	
atg ttg att gat cta atg tac aga att gcc aag ggt tac cag acc tct			5043
Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser			
1660	1665	1670	
cca gag cga ttg acc tgg ttg cag aac atg gca ggc aag cac tca gaa			5091
Pro Glu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His Ser Glu			
1675	1680	1685	1690
cga agc aat cat gct gaa gct gca cag tgt cta gtc cac tca gca gca			5139
Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val His Ser Ala Ala			
1695	1700	1705	
ctt gtt gct gaa tat ttg agc atg ctg gag gac cg ^g aaa tat ctt cct			5187
Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro			
1710	1715	1720	
gtg gga tgt gta aca ttt cag aat att tca tct aat gtt tta gaa gaa			5235
Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu			
1725	1730	1735	
tct gcg gtc tca gat gat gtg gta tct cca gat gaa gaa ggt atc tgc			5283
Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu Glu Gly Ile Cys			
1740	1745	1750	
tct gga aaa tac ttt act gag tca gga ctt gtg gga tta ctg gaa caa			5331
Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln			
1755	1760	1765	1770
gca gct gct tcc tct atg gct ggc atg tat gaa gca gtt aat gaa			5379
Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu Ala Val Asn Glu			
1775	1780	1785	
gtt tac aaa gta ctt att cct att cat gaa gct aat cg ^g gat gca aag			5427
Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn Arg Asp Ala Lys			
1790	1795	1800	
aaa cta tcc aca att cat ggt aaa ctt caa gaa gca ttc agc aaa att			5475
Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile			
1805	1810	1815	
gtt cat cag agt act ggc tgg gag cg ^g atg ttt ggc acc tat ttt cgt			5523
Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg			
1820	1825	1830	
gtt ggt ttt tat gga acc aag ttc ggg gat ttg gat gaa caa gaa ttt			5571
Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe			
1835	1840	1845	1850

gtt tac aag gag cct gca ata acc aaa ctt gca gag ata tct cac aga Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg	1855	1860	1865	5619	
ttg gag gga ttt tac gga gaa aga ttt gga gag gat gtg gtt gaa gta Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val	1870	1875	1880	5667	
atc aaa gac tct aat cct gta gac aag tgt aaa tta gat cct aac aag Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys	1885	1890	1895	5715	
gca tat att cag att acc tat gtg gag cca tac ttt gac aca tat gag Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu	1900	1905	1910	5763	
atg aag gac aga atc acc tat ttc gac aaa aat tac aat ctt cgt cga Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg	1915	1920	1925	1930	5811
ttc atg tac tgt aca ccc ttt act tta gat ggc cgt gcc cat ggg gaa Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His Gly Glu	1935	1940	1945	5859	
ctt cat gaa caa ttc aaa agg aag acc att ctg act acg tct cat gcc Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser His Ala	1950	1955	1960	5907	
ttt cct tat att aaa aca agg gtc aat gtc act cat aaa gaa gag atc Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu Glu Ile	1965	1970	1975	5955	
atc tta aca cca att gaa gtt gct att gag gac atg cag aaa aag aca Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys Lys Thr	1980	1985	1990	6003	
cag gag ttg gca ttt gca aca cat cag gat ccc gca gac ccc aaa atg Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro Lys Met	1995	2000	2005	2010	6051
ctt cag atg gta ctc cag gga tct gta ggc acc aca gtg aat cag ggg Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln Gly	2015	2020	2025	6099	
cct ttg gaa gtt gcc cag gtt ttt ctg tct gaa ata cct agt gac cca Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp Pro	2030	2035	2040	6147	
aag ctc ttc aga cat cat aat aaa ctg cga ctc tgc ttt aaa gat ttt Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe	2045	2050	2055	6195	
act aaa agg tgt gaa gat gcc tta aga aaa aat aag agc tta att ggg Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly	2060	2065	2070	6243	
ccg gtt caa aag gag tat caa agg gaa ttg ggg aaa cta tct tcg cct Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro	2075	2080	2085	2090	6291

taa agaggcccta cagccctaga tcacagaaaag tccctcagtt atccaagcca 6344

gtattgcttg tcccctgcca cagagattcc ttcagtcgaa tgagcttcg caaaatggat 6404
ctctaaactg aatgcacttg ttttattcat ctgcaaagag ccatgtattc aacatcgagt 6464
gtgaaaagat ctattggaaa ccaacatgga atggaattct ggaaattatt attcattgaa 6524
gaatgcagtg gccaagaaaa tatcaaatgt agattgttaa cgcttgagaa tcatggctat 6584
ggtttctaat gttcgggtaa caagctgtta tcttttaaga cattttatg actcaaaggt 6644
acactataca tttaccatta ttataccat agctaagggt aaaaatttat tcactttaag 6704
ttcgtatTTT ttaatttata tcaccatTTA tagattcatt ttggaccat tttaatgta 6764
gtaatgctta tttaaaggt actaaaaat atgtaatgt ttacctcgTG cgcccgagg 6824
cctc 6828

<210> 2

<211> 2090

<212> PRT

<213> Homo sapiens

<223> full-length human CLASP-3

<400> 2

Met Ala Glu Arg Arg Ala Phe Ala Gln Lys Ile Ser Arg Thr Val Ala
1 5 10 15

Ala Glu Val Arg Lys Gln Ile Ser Gly Gln Tyr Ser Gly Ser Pro Gln
20 25 30

Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr
35 40 45

Val Pro Leu Thr Glu Ala Val Asp Pro Val Asp Leu Glu Asp Tyr Leu
50 55 60

Ile Thr His Pro Leu Ala Val Asp Ser Gly Pro Leu Arg Asp Leu Ile
65 70 75 80

Glu Phe Pro Pro Asp Asp Ile Glu Val Val Tyr Ser Pro Arg Asp Cys
85 90 95

Arg Thr Leu Val Ser Ala Val Pro Glu Glu Ser Glu Met Asp Pro His
100 105 110

Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu Asp Trp Ala Ile Val Ile
115 120 125

Arg Lys Tyr His Lys Leu Gly Thr Gly Phe Asn Pro Asn Thr Leu Asp
130 135 140

Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro Lys Gln Val Phe Glu Ser
145 150 155 160

Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln Asp Asp Gln Asp Asp Leu
165 170 175

Lys Arg Arg Ser Met Ser Ile Asp Asp Thr Pro Arg Gly Ser Trp Ala
 180 185 190

 Cys Ser Ile Phe Asp Leu Lys Asn Ser Leu Pro Asp Ala Leu Leu Pro
 195 200 205

 Asn Leu Leu Asp Arg Thr Pro Asn Glu Glu Ile Asp Arg Gln Asn Asp
 210 215 220

 Asp Gln Arg Lys Ser Asn Arg His Lys Glu Leu Phe Ala Leu His Pro
 225 230 240

 Ser Pro Asp Glu Glu Pro Ile Glu Arg Leu Ser Val Pro Asp Ile
 245 250 255

 Pro Lys Glu His Phe Gly Gln Arg Leu Leu Val Lys Cys Leu Ser Leu
 260 265 270

 Lys Phe Glu Ile Glu Ile Glu Pro Ile Phe Ala Ser Leu Ala Leu Tyr
 275 280 285

 Asp Val Lys Glu Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu
 290 295 300

 Asn Ser Glu Gln Met Lys Gly Leu Leu Arg Pro His Val Pro Pro Ala
 305 310 320

 Ala Ile Thr Thr Leu Ala Arg Ser Ala Ile Phe Ser Ile Thr Tyr Pro
 325 330 335

 Ser Gln Asp Val Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln
 340 345 350

 Gly Asp Ile Gly Glu Cys Ala Glu Pro Tyr Met Ile Phe Lys Glu Ala
 355 360 365

 Asp Ala Thr Lys Asn Lys Glu Lys Leu Glu Lys Leu Lys Ser Gln Ala
 370 375 380

 Asp Gln Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp
 385 390 395 400

 Thr Ala Ile His Leu Met Asn Ile Val Ser Ser Ala Gly Ser Leu Glu
 405 410 415

 Arg Asp Ser Thr Glu Val Glu Ile Ser Thr Gly Glu Arg Lys Gly Ser
 420 425 430

 Trp Ser Glu Arg Arg Asn Ser Ser Ile Val Gly Arg Arg Ser Leu Glu
 435 440 445

 Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn Leu Thr Ser Phe Arg Pro
 450 455 460

 Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Gly Asp Arg Leu
 465 470 475 480

 Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala Asp Met Arg Arg Pro Ser
 485 490 495

Ser Val Leu Arg Arg Leu Arg Pro Ile Thr Ala Gln Leu Lys Ile Asp
 500 505 510

 Ile Ser Pro Ala Pro Glu Asn Pro His Tyr Cys Leu Thr Pro Glu Leu
 515 520 525

 Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg Val Arg Pro Thr Arg Glu
 530 535 540

 Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr Val Pro Asn Thr Thr Tyr
 545 550 555 560

 Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser Leu Asn Phe Ala Asn Arg
 565 570 575

 Gln Gly Ser Ala Arg Asn Ile Thr Val Lys Val Gln Phe Met Tyr Gly
 580 585 590

 Glu Asp Pro Ser Asn Ala Met Pro Val Ile Phe Gly Lys Ser Ser Cys
 595 600 605

 Ser Glu Phe Ser Lys Glu Ala Tyr Thr Ala Val Val Tyr His Asn Arg
 610 615 620

 Ser Pro Asp Phe His Glu Glu Ile Lys Val Lys Leu Pro Ala Thr Leu
 625 630 635 640

 Thr Asp His His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys Gln
 645 650 655

 Gln Lys Gln Asn Thr Pro Leu Glu Thr Pro Val Gly Tyr Thr Trp Ile
 660 665 670

 Pro Met Leu Gln Asn Gly Arg Leu Lys Thr Gly Gln Phe Cys Leu Pro
 675 680 685

 Val Ser Leu Glu Lys Pro Pro Gln Ala Tyr Ser Val Leu Ser Pro Glu
 690 695 700

 Val Pro Leu Pro Gly Met Lys Trp Val Asp Asn His Lys Gly Val Phe
 705 710 715 720

 Asn Val Glu Val Val Ala Val Ser Ser Ile His Thr Gln Asp Pro Tyr
 725 730 735

 Leu Asp Lys Phe Phe Ala Leu Val Asn Ala Leu Asp Glu His Leu Phe
 740 745 750

 Pro Val Arg Ile Gly Asp Met Arg Ile Met Glu Asn Asn Leu Glu Asn
 755 760 765

 Glu Leu Lys Ser Ser Ile Ser Ala Leu Asn Ser Ser Gln Leu Glu Pro
 770 775 780

 Val Val Arg Phe Leu His Leu Leu Leu Asp Lys Leu Ile Leu Leu Val
 785 790 795 800

 Ile Arg Pro Pro Val Ile Ala Gly Gln Ile Val Asn Leu Gly Gln Ala
 805 810 815

Ser Phe Glu Ala Met Ala Ser Ile Ile Asn Arg Leu His Lys Asn Leu
 820 825 830
 Glu Gly Asn His Asp Gln His Gly Arg Asn Ser Leu Leu Ala Ser Tyr
 835 840 845
 Ile His Tyr Val Phe Arg Leu Pro Asn Thr Tyr Pro Asn Ser Ser Ser
 850 855 860
 Pro Gly Pro Gly Gly Leu Gly Gly Ser Val His Tyr Ala Thr Met Ala
 865 870 875 880
 Arg Ser Ala Val Arg Pro Ala Ser Leu Asn Leu Asn Arg Ser Arg Ser
 885 890 895
 Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly Thr Pro Thr Ser Pro Asp
 900 905 910
 Asp Glu Val Arg Ser Ile Ile Gly Ser Lys Gly Leu Asp Arg Ser Asn
 915 920 925
 Ser Trp Val Asn Thr Gly Gly Pro Lys Ala Ala Pro Trp Gly Ser Asn
 930 935 940
 Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala Met Asp Arg Ser Cys Asn
 945 950 955 960
 Arg Met Ser Ser His Thr Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr
 965 970 975
 Gly Arg Leu Pro Thr Lys Lys Leu Phe His Glu Glu Leu Ala Leu Gln
 980 985 990
 Trp Val Val Cys Ser Gly Ser Val Arg Glu Ser Ala Leu Gln Gln Ala
 995 1000 1005
 Trp Phe Phe Phe Glu Leu Met Val Lys Ser Met Val His His Leu Tyr
 1010 1015 1020
 Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg
 1025 1030 1035 1040
 Phe Met Asp Asp Ile Ala Ala Leu Val Ser Thr Ile Ala Ser Asp Ile
 1045 1050 1055
 Val Ser Arg Phe Gln Lys Asp Thr Glu Met Val Glu Arg Leu Asn Thr
 1060 1065 1070
 Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu Ser Val Met Asp Arg Gly
 1075 1080 1085
 Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys
 1090 1095 1100
 Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu Val Ser Leu Arg Leu Asp
 1105 1110 1115 1120
 Phe Leu Arg Ile Ile Cys Ser His Glu His Tyr Val Thr Leu Asn Leu
 1125 1130 1135

Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser Pro Ser Pro Ser Val Ser
 1140 1145 1150
 Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser Thr Asn Val Gln Asp Gln
 1155 1160 1165
 Lys Ile Ala Asn Met Phe Glu Leu Ser Val Pro Phe Arg Gln Gln His
 1170 1175 1180
 Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu Ala Val Ile Leu Asp Pro
 1185 1190 1195 1200
 Asp Ala Glu Gly Leu Phe Gly Leu His Lys Lys Val Ile Asn Met Val
 1205 1210 1215
 His Asn Leu Leu Ser Ser His Asp Ser Asp Pro Arg Tyr Ser Asp Pro
 1220 1225 1230
 Gln Ile Lys Ala Arg Val Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile
 1235 1240 1245
 Ile Met Glu Thr Val Pro Gln Leu Tyr Asp Phe Thr Glu Thr His Asn
 1250 1255 1260
 Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu
 1265 1270 1275 1280
 Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr
 1285 1290 1295
 Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr
 1300 1305 1310
 Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu
 1315 1320 1325
 Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu
 1330 1335 1340
 Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu
 1345 1350 1355 1360
 Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys
 1365 1370 1375
 Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met
 1380 1385 1390
 Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln
 1395 1400 1405
 Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly
 1410 1415 1420
 Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr
 1425 1430 1435 1440
 His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile
 1445 1450 1455

Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu
 1460 1465 1470
 Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr
 1475 1480 1485
 Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His
 1490 1495 1500
 Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala
 1505 1510 1515 1520
 Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu
 1525 1530 1535
 Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys
 1540 1545 1550
 Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr
 1555 1560 1565
 Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val
 1570 1575 1580
 Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln
 1585 1590 1595 1600
 Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr
 1605 1610 1615
 Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln
 1620 1625 1630
 Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val
 1635 1640 1645
 Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met
 1650 1655 1660
 Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp
 1665 1670 1675 1680
 Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu
 1685 1690 1695
 Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu
 1700 1705 1710
 Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe
 1715 1720 1725
 Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp
 1730 1735 1740
 Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr
 1745 1750 1755 1760
 Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser
 1765 1770 1775

Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile
 1780 1785 1790
 Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His
 1795 1800 1805
 Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly
 1810 1815 1820
 Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr
 1825 1830 1835 1840
 Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala
 1845 1850 1855
 Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly
 1860 1865 1870
 Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro
 1875 1880 1885
 Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr
 1890 1895 1900
 Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr
 1905 1910 1915 1920
 Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro
 1925 1930 1935
 Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys
 1940 1945 1950
 Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr
 1955 1960 1965
 Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu
 1970 1975 1980
 Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala
 1985 1990 1995 2000
 Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln
 2005 2010 2015
 Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln
 2020 2025 2030
 Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His
 2035 2040 2045
 Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp
 2050 2055 2060
 Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr
 2065 2070 2075 2080
 Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro
 2085 2090

```

<210> 3
<400> 3
000
<210> 4
<400> 4
000
<210> 5
<400> 5
000
<210> 6
<400> 6
000
<210> 7
<211> 4144
<212> DNA
<213> Homo sapiens

<220>
<223> preliminary CLASP-3 cDNA

<220>
<221> CDS
<222> (2)..(3610)

<400> 7
a cga gta aat cgt tct cga agc ctt agt aat agc aat cca gat ata tct 49
  Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp Ile Ser
    1       5          10          15

ggg act ccc acg tca cca gat gat gaa gtt cga tca atc atc ggg agt  97
  Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile Gly Ser
    20      25          30

aag ggt tta gat cgc tcc aat tcc tgg gtt aac act ggt ggt cca aaa 145
  Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly Pro Lys
    35      40          45

gct gcc cca tgg gga tcc aac ccc agt cca agt gca gaa tca aca cag 193
  Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser Thr Gln
    50      55          60

gct atg gat cga agt tgt aat cgt atg tct tcg cac aca gag acg tca 241
  Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu Thr Ser
    65      70          75          80

agt ttc tta caa aca tta acg gga cgc tta cca act aaa aag ctt ttt 289
  Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys Leu Phe
    85      90          95

```

cac gag gag ctg gct ttg cag tgg gtt gtt tgc agt ggc agc gtt cgg		337	
His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser Val Arg			
100	105	110	
gaa tca gct ttg caa caa gcc tgg ttc ttt ttt gaa tta atg gta aag		385	
Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Glu Leu Met Val Lys			
115	120	125	
agc atg gtg cac cat tta tac ttt aat gat aaa ctt gag gct cca agg		433	
Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala Pro Arg			
130	135	140	
aaa agt cgt ttt cca gaa cgt ttc atg gat gac att gca gct ctt gtc		481	
Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala Leu Val			
145	150	155	160
agc acg att gct agt gat ata gtt tca cga ttt cag aag gac aca gaa		529	
Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp Thr Glu			
165	170	175	
atg gtt gag aga ctc aat aca agc ctt gca ttc ttt ctc aat gat ctg		577	
Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn Asp Leu			
180	185	190	
ttg tct gtt atg gac aga gga ttt gtt ttt agc ctt ata aag tcc tgc		625	
Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys Ser Cys			
195	200	205	
tat aaa cag gtg tct tca aag ctt tac tca tta ccg aat ccc agt gtt		673	
Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro Ser Val			
210	215	220	
ctg gtg tcc ttg agg ctg gat ttt cta cga atc atc tgc agt cat gag		721	
Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser His Glu			
225	230	235	240
cac tat gtt aca tta aac tta ccc tgc agc tta ctt act cca cct gca		769	
His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro Pro Ala			
245	250	255	
tct cca tca cct tct gtt tct gca aca tct cag agt tct gga ttt		817	
Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser Gly Phe			
260	265	270	
tct acg aat gta caa gac caa aag att gca aat atg ttt gaa tta tcc		865	
Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu Leu Ser			
275	280	285	
gtg cct ttc cgc caa cag cat tat ttg gca gga ctt gtg tta aca gag		913	
Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu Thr Glu			
290	295	300	
ctg gct gtc att tta gac cct gat gct gaa gga ctg ttt gga ttg cat		961	
Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly Leu His			
305	310	315	320
aag aaa gtc atc aat atg gta cac aat tta ctc tcc agt cac gac tca		1009	
Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His Asp Ser			
325	330	335	

gac ccg cg	tac tct gac cct cag	ata aag gct cga gtg gcc atg ttg	1057
Asp Pro Arg	Tyr Ser Asp Pro Gln	Ile Lys Ala Arg Val Ala Met Leu	
340	345	350	
tat cta cct ctg att ggt att atc atg gaa act gta cct cag ctg tat	1105		
Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln Leu Tyr			
355	360	365	
gat ttt aca gaa act cac aat caa cga gga aga cca att tgt ata gcc	1153		
Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys Ile Ala			
370	375	380	
act gat gat tat gaa agt gag agc gga agt atg ata agc cag acc gtt	1201		
Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln Thr Val			
385	390	395	400
gcc atg gca atc gca ggg aca tcg gtc cct caa cta aca agg cct ggc	1249		
Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg Pro Gly			
405	410	415	
agt ttc ctc ctc acg tca acg agt ggc agg caa cac act acc ttt tca	1297		
Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr Phe Ser			
420	425	430	
gca gaa tca agt cga agc ctt ttg atc tgt cta ctt tgg gtt ctc aaa	1345		
Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val Leu Lys			
435	440	445	
aat gca gat gaa aca gtt cta cag aag tgg ttt aca gat ctc tca gtc	1393		
Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu Ser Val			
450	455	460	
ttg cag cta aac cgg cta tta gat ctg ctt tat ctc tgt gtg tct tgc	1441		
Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val Ser Cys			
465	470	475	480
ttt gag tat aaa ggg aaa aaa gtg ttt gaa cga atg aat agc ttg acc	1489		
Phe Glu Tyr Lys Gly Lys Val Phe Glu Arg Met Asn Ser Leu Thr			
485	490	495	
ttt aag aaa tca aaa gac atg aga gca aag ctt gaa gaa gct att ctt	1537		
Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala Ile Leu			
500	505	510	
ggg agc ata ggt gcc agg caa gaa atg gta cgg cga agc cga gga cag	1585		
Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg Gly Gln			
515	520	525	
ctc gag aga agc cca tct gga agt gcc ttt gga agt caa gaa aat ttg	1633		
Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu Asn Leu			
530	535	540	
agg tgg agg aaa gat atg act cac tgg cgt caa aac aca gag aag ctt	1681		
Arg Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu Lys Leu			
545	550	555	560
gac aaa tca aga gca gag att gaa cac gaa gca ctg att gat gga aac	1729		
Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp Gly Asn			
565	570	575	

ctg gct aca gaa gca aac cta atc att tta gat aca tta gag att gtt		1777
Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu Ile Val		
580	585	590
gtt cag acc gtt tct gta acg gaa tcc aaa gag agc att ctt ggt gga		1825
Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu Gly Gly		
595	600	605
gtg cta aaa gtg cta cta cac agc atg gcc tgt aac caa agt gca gtt		1873
Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser Ala Val		
610	615	620
tat cta caa cac tgt ttt gct aca cag aga gcc ttg gtt tca aag ttt		1921
Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser Lys Phe		
625	630	635
cct gaa ctc tta ttt gaa gaa gag aca gag cag tgt gct gat tta tgc		1969
Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp Leu Cys		
645	650	655
ctc agg ctt ctc cga cac tgt agc agt agc atc ggt aca ata cgg tca		2017
Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile Arg Ser		
660	665	670
cac ccc agt gcc tcc ctt tac cta cta atg agg caa aac ttt gag att		2065
His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile		
675	680	685
ggg aat aac ttt gcc agg gtt aaa atg cag gta cca atg tca cta tcc		2113
Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser Leu Ser		
690	695	700
tcc ttg gtg ggc aca tct cag aat ttt aat gaa gaa ttc tta aga cgt		2161
Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu Arg Arg		
705	710	715
tct cta aag act ata ttg aca tat gct gaa gaa gat ctg gaa ttg agg		2209
Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu Leu Arg		
725	730	735
gaa aca aca ttt cct gat cag gtc cag gat ctg gtt ttc aat ctc cat		2257
Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn Leu His		
740	745	750
atg att ctt tct gat act gtg aaa atg aag gaa cac cag gag gat cct		2305
Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu Asp Pro		
755	760	765
gaa atg ttg att gat cta atg tac aga att gcc aag ggt tac cag acc		2353
Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr Gln Thr		
770	775	780
tct cca gat ctg cga ttg acc tgg ttg cag aac atg gca ggc aag cac		2401
Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His		
785	790	795
tca gaa cga agc aat cat gct gaa gct gca cag tgt cta gtc cac tca		2449
Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val His Ser		
805	810	815

gca gca ctt gct gaa tat ttg agc atg ctg gag gac cg ^g aaa tat Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg Lys Tyr 820 825 830	2497
ctt cct gtg gga t ^{gt} gta aca ttt cag aat att tca tct aat gtt tta Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn Val Leu 835 840 845	2545
gaa gaa tct gc ^g gtc tca gat gat gtg gta tct cca gat gaa gaa ggt Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu Glu Gly 850 855 860	2593
atc tgc tct gga aaa tac ttt act gag tca gga ctt gtg gga tta ctg Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu 865 870 875 880	2641
gaa caa gca gct gct tcc ttc tct atg gct ggc atg tat gaa gca gtt Glu Gln Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu Ala Val 885 890 895	2689
aat gaa gtt tac aaa gta ctt att cct att cat gaa gct aat cg ^g gat Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn Arg Asp 900 905 910	2737
gca aag aaa cta tcc aca att cat ggt aaa ctt caa gaa gca ttc agc Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala Phe Ser 915 920 925	2785
aaa att gtt cat cag agt act ggc tgg gag cg ^g atg ttt ggc acc tat Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly Thr Tyr 930 935 940	2833
ttt cgt gtt ggt ttt tat gga acc aag ttc ggg gat ttg gat gaa caa Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln 945 950 955 960	2881
gaa ttt gtt tac aag gag cct gca ata acc aaa ctt gca gag ata tct Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser 965 970 975	2929
cac aga ttg gag gga ttt tac gga gaa aga ttt gga gag gat gtg gtt His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp Val Val 980 985 990	2977
gaa gta atc aaa gac tct aat cct gta gac aag t ^{gt} aaa tta gat cct Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro 995 1000 1005	3025
aac aag gca tat att cag att acc tat gtg gag cca tac ttt gac aca Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr 1010 1015 1020	3073
tat gag atg aag gac aga atc acc tat ttc gac aaa aat tac aat ctt Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu 1025 1030 1035 1040	3121
cgt cga ttc atg tac t ^{gt} aca ccc ttt act tta gat ggc cgt gcc cat Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His 1045 1050 1055	3169

ggg gaa ctt cat gaa caa ttc aaa agg aag acc att ctg act acg tct		3217	
Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser			
1060	1065	1070	
cat gcc ttt cct tat att aaa aca agg gtc aat gtc act cat aaa gaa		3265	
His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu			
1075	1080	1085	
gag atc atc tta aca cca att gaa gtt gct att gag gac atg cag aaa		3313	
Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys			
1090	1095	1100	
aag aca cag gag ttg gca ttt gca aca cat cag gat ccc gca gac ccc		3361	
Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro			
1105	1110	1115	1120
aaa atg ctt cag atg gta ctc cag gga tct gta ggc acc aca gtg aat		3409	
Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn			
1125	1130	1135	
cag ggg cct ttg gaa gtt gcc cag gtt ttt ctg tct gaa ata cct agt		3457	
Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser			
1140	1145	1150	
gac cca aag ctc ttc aga cat cat aat aaa ctg cga ctc tgc ttt aaa		3505	
Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys			
1155	1160	1165	
gat ttt act aaa agg tgt gaa gat gcc tta aga aaa aat aag agc tta		3553	
Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu			
1170	1175	1180	
att ggg ccg gtt caa aag gag tat caa agg gaa ttg ggg aaa cta tct		3601	
Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys Leu Ser			
1185	1190	1195	1200
tcg cct taa agaggcccta cagccctaga tcacagaaag tccctcagtt		3650	
Ser Pro			
atccaagcca gtattgcttg tcccctgccca cagagattcc ttcagtcgaa tgagcttcg	3710		
caaaatggat ctctaaactg aatgcacttg ttttattcat ctgcaaagag ccatgtattc	3770		
aacatcgagt gtaaaaagat ctattggaaa ccaacatgga atgaaattct ggaaattatt	3830		
attcattgaa gaatgcagtg gccaagaaaa tatcaaatgt agattgttaa cgcttgagaa	3890		
tcatggctat ggttctaat gttcggtaa caagctgtta tcttttaaga cattttaatg	3950		
actcaaaggta acactataca tttaccatta tttataccat agctaaggtt aaaaatttat	4010		
tcactttaag ttcttatttt ttaatttata tcaccattta tagattcatt ttggaccat	4070		
ttaaatgta gtaatgctta ttttaaaggt actaaaaat atgtgaatgt ttacctcgtg	4130		
cgcgccaggg cctc		4144	

<210> 8
<211> 1202
<212> PRT
<213> Homo sapiens
<223> preliminary CLASP-3

<400> 8
Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp Ile Ser
1 5 10 15

Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile Gly Ser
20 25 30

Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly Pro Lys
35 40 45

Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser Thr Gln
50 55 60

Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu Thr Ser
65 70 75 80

Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys Leu Phe
85 90 95

His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser Val Arg
100 105 110

Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met Val Lys
115 120 125

Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala Pro Arg
130 135 140

Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala Leu Val
145 150 155 160

Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp Thr Glu
165 170 175

Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn Asp Leu
180 185 190

Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys Ser Cys
195 200 205

Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro Ser Val
210 215 220

Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser His Glu
225 230 235 240

His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro Pro Ala
245 250 255

Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser Gly Phe
260 265 270

Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu Leu Ser
275 280 285

Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu Thr Glu
 290 295 300
 Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly Leu His
 305 310 315 320
 Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His Asp Ser
 325 330 335
 Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala Met Leu
 340 345 350
 Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln Leu Tyr
 355 360 365
 Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys Ile Ala
 370 375 380
 Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln Thr Val
 385 390 395 400
 Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg Pro Gly
 405 410 415
 Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr Phe Ser
 420 425 430
 Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val Leu Lys
 435 440 445
 Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu Ser Val
 450 455 460
 Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val Ser Cys
 465 470 475 480
 Phe Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser Leu Thr
 485 490 495
 Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala Ile Leu
 500 505 510
 Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg Gly Gln
 515 520 525
 Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu Asn Leu
 530 535 540
 Arg Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu Lys Leu
 545 550 555 560
 Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp Gly Asn
 565 570 575
 Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu Ile Val
 580 585 590
 Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu Gly Gly
 595 600 605

Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser Ala Val
 610 615 620
 Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser Lys Phe
 625 630 635 640
 Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp Leu Cys
 645 650 655
 Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile Arg Ser
 660 665 670
 His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile
 675 680 685
 Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser Leu Ser
 690 695 700
 Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu Arg Arg
 705 710 715 720
 Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu Leu Arg
 725 730 735
 Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn Leu His
 740 745 750
 Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu Asp Pro
 755 760 765
 Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr Gln Thr
 770 775 780
 Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His
 785 790 795 800
 Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val His Ser
 805 810 815
 Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg Lys Tyr
 820 825 830
 Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn Val Leu
 835 840 845
 Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu Glu Gly
 850 855 860
 Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu
 865 870 875 880
 Glu Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu Ala Val
 885 890 895
 Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn Arg Asp
 900 905 910
 Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala Phe Ser
 915 920 925

Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly Thr Tyr
 930 935 940
 Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
 945 950 955 960
 Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser
 965 970 975
 His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp Val Val
 980 985 990
 Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro
 995 1000 1005
 Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr
 1010 1015 1020
 Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu
 1025 1030 1035 1040
 Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His
 1045 1050 1055
 Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser
 1060 1065 1070
 His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu
 1075 1080 1085
 Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys
 1090 1095 1100
 Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro
 1105 1110 1115 1120
 Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn
 1125 1130 1135
 Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser
 1140 1145 1150
 Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys
 1155 1160 1165
 Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu
 1170 1175 1180
 Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys Leu Ser
 1185 1190 1195 1200
 Ser Pro

<210> 9
 <211> 1352
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-2

<400> 9
 Val Leu His His His Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile
 1 5 10 15

 Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe
 20 25 30

 Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg
 35 40 45

 Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys
 50 55 60

 Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn
 65 70 75 80

 Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His
 85 90 95

 Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys
 100 105 110

 Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu
 115 120 125

 His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala
 130 135 140

 Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu
 145 150 155 160

 Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe
 165 170 175

 Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr
 180 185 190

 Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu
 195 200 205

 Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr
 210 215 220

 Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met
 225 230 235 240

 Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu
 245 250 255

 Leu Arg Tyr Ser Trp Phe Phe Asp Val Leu Ile Lys Ser Met Ala
 260 265 270

 Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg
 275 280 285

 Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn Met Leu
 290 295 300

 Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala Ser Lys
 305 310 315 320

Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys	Phe	Thr	Phe
				325					330				335		
Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr	Ile	Ser	Cys
				340				345				350			
Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	Lys	Phe	Glu	Phe
				355				360				365			
Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro
				370				375				380			
Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	Asp	Leu	Gln	Leu
				385				390				395			400
Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe	Leu	Val	Gly
				405					410				415		
Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	Arg	Glu	Val
				420				425				430			
Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile	Lys	His	Ser
				435				440				445			
Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg	Ile	Ala	Thr
				450				455				460			
Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val	Gln	Arg	Ile
				465				470				475			480
Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly	Met	Thr	Val
				485					490				495		
Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu	Val	Thr	Pro
				500				505				510			
Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	Leu	Leu	Gly
				515				520				525			
Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr	Pro	Asn	Ile
				530				535				540			
Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Ser	Thr	Asp
				545				550				555			560
Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys	Ser	Asn	Ser	Leu
				565					570				575		
Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser	Val	Val	Arg	Cys
				580				585				590			
Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	Cys	Phe	Leu
				595				600				605			
Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	Tyr	Trp	Asn
				610				615				620			
Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile	Ser	Glu	Val
				625				630				635			640

Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala Arg Asn
 645 650 655

 Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln Thr Leu
 660 665 670

 Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu Gln Gln
 675 680 685

 Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His
 690 695 700

 Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala
 705 710 720

 Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu
 725 730 735

 Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met
 740 745 750

 Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser
 755 760 765

 Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr
 770 775 780

 Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala
 785 790 800

 Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile
 805 810 815

 Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe
 820 825 830

 Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile
 835 840 845

 Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr
 850 855 860

 Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp
 865 870 880

 Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr
 885 890 895

 Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His
 900 905 910

 Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys
 915 920 925

 Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met
 930 935 940

 Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys
 945 950 955 960

Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly
 965 970 975

Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile
 980 985 990

Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His
 995 1000 1005

Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly
 1010 1015 1020

Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu
 1025 1030 1035 1040

Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp Glu Asp
 1045 1050 1055

Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu
 1060 1065 1070

Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu
 1075 1080 1085

Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu
 1090 1095 1100

Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe
 1105 1110 1115 1120

Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His
 1125 1130 1135

Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys
 1140 1145 1150

Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr
 1155 1160 1165

Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr
 1170 1175 1180

Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met
 1185 1190 1195 1200

Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val
 1205 1210 1215

Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln
 1220 1225 1230

Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr
 1235 1240 1245

Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val
 1250 1255 1260

Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu
 1265 1270 1275 1280

Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala
1285 1290 1295

Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln
1300 1305 1310

Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His
1315 1320 1325

Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly
1330 1335 1340

Met Thr Ser Ser Ser Ser Val Val
1345 1350

<210> 10

<211> 1534

<212> PRT

<213> Homo sapiens

<220>

<223> KIAA1058

<400> 10

Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg
1 5 10 15

Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
20 25 30

Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
35 40 45

Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
50 55 60

Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
65 70 75 80

Thr Pro Ile Thr Phe Glu Val Glu Phe Val Pro Cys Ile Pro Lys
85 90 95

His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
100 105 110

Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
115 120 125

Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
130 135 140

Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
145 150 155 160

Ser Ala Phe Ala Ala Val Leu His His Gln Asn Pro Glu Phe Tyr
165 170 175

Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
180 185 190

Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
 195 200 205
 Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
 210 215 220
 Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
 225 230 235 240
 Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
 245 250 255
 Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly
 260 265 270
 Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr
 275 280 285
 Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu
 290 295 300
 Ser Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser
 305 310 315 320
 Leu His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile
 325 330 335
 Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val
 340 345 350
 Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His
 355 360 365
 Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr
 370 375 380
 Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu
 385 390 395 400
 Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu
 405 410 415
 Thr Ser Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Asp Val Leu
 420 425 430
 Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu
 435 440 445
 Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Val Glu Thr
 450 455 460
 Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Arg Asp Asn
 465 470 475 480
 Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys
 485 490 495
 Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn
 500 505 510

Asn	Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu
515							520					525			
Tyr	Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile
530					535						540				
Pro	Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr
545					550				555			560			
Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn
					565				570			575			
His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln
					580				585			590			
Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu
					595		600				605				
Leu	Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln
					610		615				620				
Ala	Arg	Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu
					625		630				635			640	
Asn	Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn
					645				650			655			
Ala	Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn
					660			665			670				
Pro	Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His
					675		680				685				
Lys	Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr
					690		695				700				
Ser	Thr	Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser
					705		710				715			720	
Leu	Ile	Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu
					725				730			735			
Lys	Ser	Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn
					740			745			750				
Ser	Val	Val	Arg	Cys	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu
					755		760				765				
Leu	Met	Cys	Phe	Leu	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu
					770		775				780				
Phe	Thr	Tyr	Trp	Asn	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe
					785		790				795			800	
Thr	Ile	Ser	Glu	Val	Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg
					805			810			815				
Tyr	Ile	Ala	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln	Leu	Gly
					820		825				830				

Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
 835 840 845
 Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
 850 855 860
 Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
 865 870 875 880
 Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
 885 890 895
 Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
 900 905 910
 Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
 915 920 925
 Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
 930 935 940
 Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
 945 950 955 960
 Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
 965 970 975
 Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
 980 985 990
 Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
 995 1000 1005
 Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
 1010 1015 1020
 Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
 1025 1030 1035 1040
 Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
 1045 1050 1055
 Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
 1060 1065 1070
 Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
 1075 1080 1085
 Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
 1090 1095 1100
 His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
 1105 1110 1115 1120
 Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg
 1125 1130 1135
 Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
 1140 1145 1150

Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly
 1155 1160 1165

 Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
 1170 1175 1180

 Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
 1185 1190 1195 1200

 Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
 1205 1210 1215

 Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
 1220 1225 1230

 Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
 1235 1240 1245

 Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
 1250 1255 1260

 Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
 1265 1270 1275 1280

 Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
 1285 1290 1295

 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
 1300 1305 1310

 Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
 1315 1320 1325

 Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
 1330 1335 1340

 Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
 1345 1350 1355 1360

 Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
 1365 1370 1375

 Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
 1380 1385 1390

 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 1395 1400 1405

 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 1410 1415 1420

 Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 1425 1430 1435 1440

 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 1445 1450 1455

 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 1460 1465 1470

Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
1475 1480 1485

Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
1490 1495 1500

Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
1505 1510 1515 1520

Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly
1525 1530

<210> 11

<211> 738

<212> PRT

<213> Rattus norvegicus

<220>

<223> rat TRG

<400> 11

Lys Leu Ser Arg Gly His Ser Pro Leu Met Lys Lys Val Phe Asp Val
1 5 10 15

Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn
20 25 30

Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe
35 40 45

Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu
50 55 60

Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln
65 70 75 80

Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys
85 90 95

Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu
100 105 110

Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu
115 120 125

Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr
130 135 140

Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val
145 150 155 160

Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met
165 170 175

Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro
180 185 190

Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys
195 200 205

Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala
 210 215 220
 Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Asp Leu Ala Leu Gln
 225 230 235 240
 Arg Glu Pro Pro Val Phe Pro Tyr Ser His Thr Ser Cys Gln Arg Lys
 245 250 255
 Ser Arg Gly Gly Met Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 260 265 270
 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 275 280 285
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
 290 295 300
 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Leu Arg Ala Gly Leu Leu
 305 310 315 320
 Thr Ser Ile Asn Ser Ser Pro Ser Met Lys Ser Gly Gly Thr Leu
 325 330 335
 Glu Thr Thr His Leu Tyr Asp Thr Leu His Arg Pro Tyr Ser Lys Val
 340 345 350
 Thr Glu Val Ile Thr Arg Ala Ala Gly Ser Trp Asp Leu Leu Pro Gly
 355 360 365
 Gly Leu Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
 370 375 380
 Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
 385 390 395 400
 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
 405 410 415
 Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe
 420 425 430
 Ala Tyr Ile Gln Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
 435 440 445
 Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Cys His Asn Ile Arg Arg
 450 455 460
 Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
 465 470 475 480
 Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
 485 490 495
 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 500 505 510
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 515 520 525

Ala Glu Leu His Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 530 535 540
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 545 550 555 560
 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 565 570 575
 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 580 585 590
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 595 600 605
 Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 610 615 620
 Ile Arg Lys Glu Leu Ser Asp Ile Ile Val Pro Arg Ile Cys Pro Gly
 625 630 635 640
 Glu Asp Lys Arg Ala Thr Lys Phe Pro Ala His Leu Gln Arg His Gln
 645 650 655
 Arg Asp Thr Asn Lys His Ser Gly Ser Arg Val Asp Gln Phe Ile Leu
 660 665 670
 Ser Cys Val Thr Leu Pro His Glu Pro His Val Gly Thr Cys Phe Val
 675 680 685
 Met Cys Lys Leu Arg Thr Thr Phe Arg Ala Asn His Trp Phe Cys Gln
 690 695 700
 Ala Gln Glu Glu Ala Met Gly Asn Gly Arg Glu Lys Glu Pro Trp Thr
 705 710 715 720
 Val Ile Phe Asn Ser Arg Phe Tyr Arg Ser Trp Gly Lys Val His Ile
 725 730 735
 Phe Phe

<210> 12
 <211> 1214
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human CLASP-4

 <400> 12
 Met Glu Ile Gln Val Leu Ile Arg Phe Leu Ser Val Ile Leu Met Gln
 1 5 10 15

 Leu Phe Trp Val Leu Pro Asn Met Ile His Glu Asp Asp Val Pro Ile
 20 25 30

 Ser Cys Pro Met Val Leu Phe His Ile Val Ser Lys Cys His Glu Glu
 35 40 45

Gly Leu Asp Ser Tyr Leu Ser Ser Phe Ile Lys Tyr Ser Phe Arg Pro
 50 55 60
 Gly Lys Pro Ser Ala Pro Gln Ala Pro Leu Ile His Glu Thr Leu Ala
 65 70 75 80
 Thr Met Met Ile Ala Leu Leu Lys Gln Ser Ala Asp Phe Leu Ala Ile
 85 90 95
 Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Glu Ile Ile Ala Lys
 100 105 110
 Ser Met Ala Thr Tyr Leu Leu Glu Glu Asn Lys Ile Lys Leu Thr His
 115 120 125
 Gly Gln Arg Phe Pro Lys Ala Tyr His His Ala Leu His Ser Leu Phe
 130 135 140
 Leu Ala Ile Thr Ile Val Glu Ser Gln Tyr Ala Glu Ile Pro Lys Glu
 145 150 155 160
 Ser Arg Asn Val Asn Tyr Ser Leu Ala Ser Phe Leu Lys Cys Cys Leu
 165 170 175
 Thr Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Asn Asp Tyr Ile
 180 185 190
 Ser Gly Phe Ser Pro Lys Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe
 195 200 205
 Glu Phe Leu Gln Thr Ile Cys Asn His Glu His Tyr Ile Pro Leu Asn
 210 215 220
 Leu Pro Met Ala Phe Ala Lys Pro Lys Leu Gln Arg Val Gln Asp Ser
 225 230 235 240
 Asn Leu Glu Tyr Ser Leu Ser Asp Glu Tyr Cys Lys His His Phe Leu
 245 250 255
 Val Gly Leu Leu Leu Arg Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr
 260 265 270
 Glu Ile Arg Tyr Thr Ala Ile Ser Val Ile Lys Asn Leu Leu Ile Lys
 275 280 285
 His Ala Phe Asp Thr Arg Tyr Gln His Lys Asn Gln Gln Ala Lys Ile
 290 295 300
 Ala Gln Leu Tyr Leu Pro Phe Val Gly Leu Leu Leu Glu Asn Ile Gln
 305 310 315 320
 Arg Leu Ala Gly Arg Asp Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn
 325 330 335
 Ser Ala Ser Arg Asp Glu Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn
 340 345 350
 Arg Gly Ser Leu Ser Thr Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln
 355 360 365

Asn Gly His Gly Ile Lys Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro
 370 375 380
 Glu Gly Ala Thr Gly Phe Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr
 385 390 395 400
 Arg Gln Ser Ser Thr Arg Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp
 405 410 415
 Gln Tyr Glu Ile Arg Ser Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys
 420 425 430
 Met Ile Ser Glu Asp Thr Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro
 435 440 445
 Gln Glu Leu Ile Asn Ile Leu Ile Leu Glu Val Cys Leu Phe His
 450 455 460
 Phe Arg Tyr Met Gly Lys Arg Asn Ile Ala Arg Val His Asp Ala Trp
 465 470 475 480
 Leu Ser Lys His Phe Gly Ile Asp Arg Lys Ser Gln Thr Met Pro Ala
 485 490 495
 Leu Arg Asn Arg Ser Gly Val Met Gln Ala Arg Leu Gln His Leu Ser
 500 505 510
 Ser Leu Glu Ser Ser Phe Thr Leu Asn His Ser Ser Thr Thr Thr Glu
 515 520 525
 Ala Asp Ile Phe His Gln Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu
 530 535 540
 Val Ser Leu Thr Val Leu Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe
 545 550 555 560
 Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys
 565 570 575
 Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val
 580 585 590
 Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe
 595 600 605
 Pro Ser Ala Phe Phe Lys Gly Arg Val Asn Met Cys Ala Ala Phe Cys
 610 615 620
 Tyr Glu Val Leu Lys Cys Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn
 625 630 635 640
 Glu Ala Ser Ala Leu Leu Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr
 645 650 655
 Thr Lys Arg Lys Thr Phe Leu Arg Thr His Leu Gln Ile Ile Ile Ala
 660 665 670
 Val Ser Gln Leu Ile Ala Asp Val Ala Leu Ser Gly Gly Ser Arg Phe
 675 680 685

Gln Glu Ser Leu Phe Ile Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro
 690 695 700
 Met Leu Ala Arg Ala Phe Pro Ala Glu Val Lys Asp Leu Thr Lys Arg
 705 710 715 720
 Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Lys
 725 730 735
 Asp Pro Glu Met Leu Ile Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
 740 745 750
 Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Lys
 755 760 765
 Ile His Val Lys Asn Gly Asp Phe Ser Glu Ala Ala Met Cys Tyr Val
 770 775 780
 His Val Ala Ala Leu Val Ala Glu Phe Leu His Arg Lys Lys Leu Phe
 785 790 795 800
 Pro Asn Gly Cys Ser Ala Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu
 805 810 815
 Glu Gly Ala Met Lys Glu Asp Ala Gly Met Met Asp Val His Tyr Ser
 820 825 830
 Glu Glu Val Leu Leu Glu Leu Leu Glu Gln Cys Val Asn Gly Leu Trp
 835 840 845
 Lys Ala Glu Arg Tyr Glu Ile Ile Ser Glu Ile Ser Lys Leu Ile Gly
 850 855 860
 Pro Ile Tyr Glu Asn Arg Arg Glu Phe Glu Asn Leu Thr Gln Val Tyr
 865 870 875 880
 Arg Thr Leu His Gly Ala Tyr Thr Lys Ile Leu Glu Val Met His Thr
 885 890 895
 Lys Lys Arg Leu Leu Gly Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln
 900 905 910
 Ser Phe Phe Glu Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
 915 920 925
 Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr
 930 935 940
 Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser Asp
 945 950 955 960
 Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln Val
 965 970 975
 Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys
 980 985 990
 Thr Glu Phe Glu Arg Asn His Asn Ile Ser Arg Phe Val Phe Glu Ala
 995 1000 1005

Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys
 1010 1015 1020

 Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys
 1025 1030 1035 1040

 Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile
 1045 1050 1055

 Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys
 1060 1065 1070

 Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu
 1075 1080 1085

 Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala
 1090 1095 1100

 Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys
 1105 1110 1115 1120

 Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser
 1125 1130 1135

 Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu
 1140 1145 1150

 Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu
 1155 1160 1165

 Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser
 1170 1175 1180

 Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr
 1185 1190 1195 1200

 Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val
 1205 1210

<210> 13
 <211> 1288
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-1

<400> 13
 Met Ser Phe Leu Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val
 1 5 10 15

 Gln Asn Glu Glu Asp Glu Ile Thr Thr Val Thr Arg Val Leu Pro
 20 25 30

 Asp Ile Val Ala Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln
 35 40 45

 Ser Tyr Ile Lys Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro
 50 55 60

Val His Glu Asp Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn
 65 70 75 80
 Asp Ser Pro Thr Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe
 85 90 95
 Ala Ile Ile Leu Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys
 100 105 110
 Ile Gln Leu Pro Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu
 115 120 125
 Leu Asp Asn Leu Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr
 130 135 140
 Lys Asp Ala Leu Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg
 145 150 155 160
 Phe Leu Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys
 165 170 175
 Met Val Asn Asn Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr
 180 185 190
 Leu Cys Gln Tyr Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu
 195 200 205
 His Phe Ile Pro Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp
 210 215 220
 Pro Leu Thr Pro Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met
 225 230 235 240
 Pro Glu Tyr Ser Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile
 245 250 255
 Gly Ile Leu Leu Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp
 260 265 270
 Val Arg His Leu Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His
 275 280 285
 Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala
 290 295 300
 Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg
 305 310 315 320
 Ile Tyr Leu Lys Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln
 325 330 335
 Gly Ser Arg Asp Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr
 340 345 350
 Ala Ile Lys His Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val
 355 360 365
 Leu Asn Ser Ile Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn
 370 375 380

His	Ala	Asp	Ser	Arg	Ala	Ser	Leu	Ala	Ser	Leu	Asp	Ser	Asn	Pro	Ser
385					390						395				400
Thr	Asn	Glu	Lys	Ser	Ser	Glu	Lys	Thr	Asp	Asn	Cys	Glu	Lys	Ile	Pro
					405					410					415
Arg	Pro	Leu	Ala	Leu	Ile	Gly	Ser	Thr	Leu	Arg	Phe	Asp	Arg	Leu	Asp
					420					425					430
Gln	Ala	Glu	Thr	Arg	Ser	Leu	Leu	Met	Cys	Phe	Leu	His	Ile	Met	Lys
					435			440				445			
Thr	Ile	Ser	Tyr	Glu	Thr	Leu	Ile	Ala	Tyr	Trp	Gln	Arg	Ala	Pro	Ser
					450			455			460				
Pro	Glu	Val	Ser	Asp	Phe	Phe	Ser	Ile	Leu	Asp	Val	Cys	Leu	Gln	Asn
					465		470			475					480
Phe	Arg	Tyr	Leu	Gly	Lys	Arg	Asn	Ile	Ile	Arg	Lys	Ile	Ala	Ala	Ala
					485				490				495		
Phe	Lys	Phe	Val	Gln	Ser	Thr	Gln	Asn	Asn	Gly	Thr	Leu	Lys	Gly	Ser
					500				505				510		
Asn	Pro	Ser	Cys	Gln	Thr	Ser	Gly	Leu	Leu	Ala	Gln	Trp	Met	His	Ser
					515			520				525			
Thr	Ser	Arg	His	Glu	Gly	His	Lys	Gln	His	Arg	Ser	Gln	Thr	Leu	Pro
					530			535				540			
Ile	Ile	Arg	Gly	Lys	Asn	Ala	Leu	Ser	Asn	Pro	Lys	Leu	Leu	Gln	Met
					545		550			555					560
Leu	Asp	Asn	Thr	Met	Thr	Ser	Asn	Ser	Asn	Glu	Ile	Asp	Ile	Val	His
					565				570				575		
His	Val	Asp	Thr	Glu	Ala	Asn	Ile	Ala	Thr	Glu	Gly	Cys	Leu	Thr	Ile
					580				585				590		
Leu	Asp	Leu	Val	Ser	Leu	Phe	Thr	Gln	Thr	His	Gln	Arg	Gln	Leu	Gln
					595			600				605			
Gln	Cys	Asp	Cys	Gln	Asn	Ser	Leu	Met	Lys	Arg	Gly	Phe	Asp	Thr	Tyr
					610		615				620				
Met	Leu	Phe	Phe	Gln	Val	Asn	Gln	Ser	Ala	Thr	Ala	Leu	Lys	His	Val
					625		630			635					640
Phe	Ala	Ser	Leu	Arg	Leu	Phe	Val	Cys	Lys	Phe	Pro	Ser	Ala	Phe	Phe
					645				650					655	
Gln	Gly	Pro	Ala	Asp	Leu	Cys	Gly	Ser	Phe	Cys	Tyr	Glu	Val	Leu	Lys
					660			665				670			
Cys	Cys	Asn	His	Arg	Ser	Arg	Ser	Thr	Gln	Thr	Glu	Ala	Ser	Ala	Leu
					675			680				685			
Leu	Tyr	Leu	Phe	Met	Arg	Lys	Asn	Phe	Glu	Phe	Asn	Lys	Gln	Lys	Ser
					690			695				700			

Ile Val Arg Ser His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile
 705 710 715 720
 Ala Asp Ala Gly Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile
 725 730 735
 Thr Asn Asn Phe Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe
 740 745 750
 Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met
 755 760 765
 Ala Thr Ala Gln Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val
 770 775 780
 Asp Leu Gln Tyr Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu
 785 790 795 800
 Arg Arg Thr Trp Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly
 805 810 815
 Asp Leu Ser Glu Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile
 820 825 830
 Ala Glu Tyr Leu Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys
 835 840 845
 Thr Ala Ser Leu Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser
 850 855 860
 Leu Leu Thr Thr Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro
 865 870 875 880
 Ala Phe Leu Ser Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys
 885 890 895
 Glu Asp Ser Gly Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val
 900 905 910
 Glu Gln Leu Tyr Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr
 915 920 925
 Glu Leu Ile Ala Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys
 930 935 940
 Gln Arg Asp Phe Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg
 945 950 955 960
 Ser Tyr Leu Lys Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe
 965 970 975
 Gly Arg Tyr Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu
 980 985 990
 Glu Glu Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu
 995 1000 1005
 Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly
 1010 1015 1020

Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys
 1025 1030 1035 1040

 Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro
 1045 1050 1055

 Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met
 1060 1065 1070

 His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser
 1075 1080 1085

 Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile
 1090 1095 1100

 Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val
 1105 1110 1115 1120

 Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp
 1125 1130 1135

 Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu
 1140 1145 1150

 Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
 1155 1160 1165

 Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu
 1170 1175 1180

 Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys
 1185 1190 1195 1200

 Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val
 1205 1210 1215

 Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu
 1220 1225 1230

 Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn
 1235 1240 1245

 Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln
 1250 1255 1260

 Thr Cys Thr Arg Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val
 1265 1270 1275 1280

 Ser Ile Ser Ser Ser Ala Glu Val
 1285

<210> 14
 <211> 1220
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-3

<400> 14
 Gly Pro Gly Pro Ala Arg Ser Thr Val Ser Ile Ser Leu Ile Ser Asn
 1 5 10 15

 Ser Ala Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp
 20 25 30

 Ile Ser Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile
 35 40 45

 Gly Ser Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly
 50 55 60

 Pro Lys Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser
 65 70 75 80

 Thr Gln Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu
 85 90 95

 Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys
 100 105 110

 Leu Phe His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser
 115 120 125

 Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met
 130 135 140

 Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala
 145 150 160

 Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala
 165 170 175

 Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp
 180 185 190

 Thr Glu Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn
 195 200 205

 Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys
 210 215 220

 Ser Cys Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro
 225 230 240

 Ser Val Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser
 245 250 255

 His Glu His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro
 260 265 270

 Pro Ala Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser
 275 280 285

 Gly Phe Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu
 290 295 300

 Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu
 305 310 315 320

Thr Glu Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly
 325 330 335
 Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His
 340 345 350
 Asp Ser Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala
 355 360 365
 Met Leu Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln
 370 375 380
 Leu Tyr Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys
 385 390 395 400
 Ile Ala Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln
 405 410 415
 Thr Val Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg
 420 425 430
 Pro Gly Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr
 435 440 445
 Phe Ser Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val
 450 455 460
 Leu Lys Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu
 465 470 475 480
 Ser Val Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val
 485 490 495
 Ser Cys Phe Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser
 500 505 510
 Leu Thr Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala
 515 520 525
 Ile Leu Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg
 530 535 540
 Gly Gln Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu
 545 550 555 560
 Asn Leu Arg Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu
 565 570 575
 Lys Leu Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp
 580 585 590
 Gly Asn Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu
 595 600 605
 Ile Val Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu
 610 615 620
 Gly Gly Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser
 625 630 635 640

Ala Val Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser
 645 650 655

 Lys Phe Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp
 660 665 670

 Leu Cys Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile
 675 680 685

 Arg Ser His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe
 690 695 700

 Glu Ile Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser
 705 710 715 720

 Leu Ser Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu
 725 730 735

 Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu
 740 745 750

 Leu Arg Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn
 755 760 765

 Leu His Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu
 770 775 780

 Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr
 785 790 795 800

 Gln Thr Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly
 805 810 815

 Lys His Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val
 820 825 830

 His Ser Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg
 835 840 845

 Lys Tyr Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn
 850 855 860

 Val Leu Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu
 865 870 875 880

 Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly
 885 890 895

 Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu
 900 905 910

 Ala Val Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn
 915 920 925

 Arg Asp Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala
 930 935 940

 Phe Ser Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly
 945 950 955 960

Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp
 965 970 975
 Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu
 980 985 990
 Ile Ser His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp
 995 1000 1005
 Val Val Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu
 1010 1015 1020
 Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe
 1025 1030 1035 1040
 Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr
 1045 1050 1055
 Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg
 1060 1065 1070
 Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr
 1075 1080 1085
 Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His
 1090 1095 1100
 Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met
 1105 1110 1115 1120
 Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala
 1125 1130 1135
 Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr
 1140 1145 1150
 Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile
 1155 1160 1165
 Pro Ser Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys
 1170 1175 1180
 Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys
 1185 1190 1195 1200
 Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys
 1205 1210 1215
 Leu Ser Ser Pro
 1220

<210> 15
 <211> 987
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-5

<400> 15
 Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys Pro Ser Ile Ser Ser
 1 5 10 15

 Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp Gln Lys Ile Ala Ser
 20 25 30

 Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser Ser Pro
 35 40 45

 Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu Gly Glu
 50 55 60

 Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His Ser Leu
 65 70 75 80

 Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu Val Lys
 85 90 95

 Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile Leu Asp
 100 105 110

 Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg Arg Tyr
 115 120 125

 Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala Ile Thr
 130 135 140

 Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu Lys Thr
 145 150 155 160

 Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn Met Leu
 165 170 175

 Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp Ile Met
 180 185 190

 Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp Leu Pro
 195 200 205

 Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys Val Leu
 210 215 220

 Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser Thr Gln
 225 230 235 240

 Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu Glu Glu Ala Leu
 245 250 255

 Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg Arg Arg Ala Pro
 260 265 270

 Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu Arg Trp Lys Lys
 275 280 285

 Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu Asp Lys Thr Lys
 290 295 300

 Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn Leu Ala Thr Glu
 305 310 315 320

Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile Ile Gln Ala Ser
 325 330 335
 Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly Val Leu Arg Val
 340 345 350
 Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr Tyr Leu Thr His
 355 360 365
 Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe Gly Asp Leu Leu
 370 375 380
 Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys His Gln Val Leu
 385 390 395 400
 His His Cys Ser Ser Met Asp Val Thr Arg Ser Gln Ala Cys Ala
 405 410 415
 Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser Asn Phe
 420 425 430
 Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala Ser Leu Val Gly
 435 440 445
 Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg Ser Leu Arg Thr
 450 455 460
 Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln Met Thr Pro Phe
 465 470 475 480
 Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn Ser Ile Leu Tyr
 485 490 495
 Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met Leu Met
 500 505 510
 Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro Asp Leu
 515 520 525
 Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys Lys Lys
 530 535 540
 Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala Leu Val
 545 550 555 560
 Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro Val Gly
 565 570 575
 Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Val
 580 585 590
 Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys Ala Gly
 595 600 605
 Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala
 610 615 620
 Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu Val Tyr
 625 630 635 640

Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg Lys Leu
 645 650 655
 Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile Val Asn
 660 665 670
 Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Phe
 675 680 685
 Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu
 690 695 700
 Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg Leu Glu Ala Phe
 705 710 720
 Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val Ile Lys Asp Ser
 725 730 735
 Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
 740 745 750
 Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys Asp Arg
 755 760 765
 Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg Phe Met Tyr Thr
 770 775 780
 Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu Leu His Glu Gln
 785 790 800
 Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile
 805 810 815
 Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro
 820 825 830
 Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
 835 840 845
 Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met Leu Gln Met Val
 850 855 860
 Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly Pro Leu Glu Val
 865 870 875 880
 Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro Lys Leu Tyr Arg
 885 890 895
 His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe Ile Met Arg Cys
 900 905 910
 Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg
 915 920 925
 Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn
 930 935 940
 Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile
 945 950 955 960

Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe
965 970 975

Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
980 985

<210> 16
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-1

<400> 16
Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 17
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from human KIAA1058

Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu
20 25 30

Tyr Ile Tyr Lys Glu Pro
35

<210> 18
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-2

<400> 18
Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
1 5 10

<210> 19
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-6

<400> 19
Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 20
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-4

<400> 20
Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 21
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK180

<400> 21
Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 22
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK2

<400> 22
Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 23
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK3

<400> 23
Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Tyr Val Cys Arg Gly His
20

<210> 24
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from human KIAA0716

<400> 24
Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Phe Val Cys Arg Gly His
20

<210> 25
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-3

<400> 25
Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
1 5 10 15

Glu Phe Val Tyr Lys Glu Pro
20

<210> 26
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from rat TRG

<400> 26
 Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
 1 5 10 15
 Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser
 20 25 30
 Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln
 35 40 45
 Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
 50 55 60

<210> 27
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human CLASP-1

<400> 27
 Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
 1 5 10 15
 Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser
 20 25 30
 Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln
 35 40 45
 Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu
 50 55 60

<210> 28
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human CLASP-2

<400> 28
 Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
 1 5 10 15
 Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
 20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
35 40 45

Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 29
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-4

<400> 29
Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu
1 5 10 15

Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser
20 25 30

Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln
35 40 45

Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu
50 55 60

<210> 30
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-3

<400> 30
Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe
1 5 10 15

Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser
20 25 30

Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
35 40 45

Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu
50 55 60

<210> 31
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from human KIAA0716

<400> 31
His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu
1 5 10 15

Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr
20 25 30

Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45

Ile Pro Glu Ser Gln Glu
50

<210> 32
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from canonical DOCK3

<400> 32
His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu
1 5 10 15

Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala
20 25 30

Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45

Ile Pro Asp Tyr Val Asp
50

<210> 33
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from canonical DOCK2

<400> 33
Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn
1 5 10 15

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr
20 25 30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro
35 40 45

<210> 34
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from canonical DOCK180

<400> 34
 Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe
 1 5 10 15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val
 20 25 30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val
 35 40 45

Leu Asp Glu His Pro
 50

<210> 35
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-1

<400> 35
 Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn
 35 40 45

<210> 36
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from rat TRG

<400> 36
 Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu His
 35 40 45

```

<210> 37
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from human KIAA1058

<400> 37
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
  1           5           10          15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
  20          25          30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
  35          40          45

<210> 38
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from human CLASP-2

<400> 38
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
  1           5           10          15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
  20          25          30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
  35          40          45

<210> 39
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from human CLASP-6

<400> 39
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
  1           5           10          15

Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
  20          25          30

His Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
  35          40

```

```

<210> 40
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from human CLASP-4

<400> 40
Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg
  1           5               10          15

.Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val
  20          25             30

Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln
  35          40             45

<210> 41
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from human CLASP-3

<400> 41
Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg
  1           5               10          15

Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val
  20          25             30

Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala
  35          40             45

<210> 42
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from human CLASP-5

<400> 42
Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg
  1           5               10          15

Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val
  20          25             30

Ala Ile Glu Asp Met Lys Lys Thr Leu Gln Leu Ala
  35          40             45

```

```

<210> 43
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from human KIAA0716

<400> 43
Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp
 1           5           10          15

Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn
 20          25          30

Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys
 35          40          45

<210> 44
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from canonical DOCK2

<400> 44
Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1           5           10          15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20          25          30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35          40          45

<210> 45
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
      and E from canonical DOCK3

<400> 45
Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp
 1           5           10          15

Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn
 20          25          30

Ala Ile Gln Val Val Glu Asn Lys Asn Gln Glu Leu Arg
 35          40          45

```

<210> 46
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK180

<400> 46
 Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

<210> 47
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from human CLASP-1

<400> 47
 Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala
 1 5 10 15

Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys
 20 25 30

Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln
 35 40 45

Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp
 50 55

<210> 48
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from rat TRG

<400> 48
 Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
 20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
 35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 49
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human KIAA1058

<400> 49
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 50
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-2

<400> 50
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 51
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-6

<400> 51
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 52
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-3

<400> 52
Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
20 25 30

Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
35 40 45

Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg
50 55

<210> 53
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-4

<400> 53
Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser
20 25 30

Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys
35 40 45

Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu
50 55

<210> 54
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F and G from human CLASP-5

<400> 54
Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp
20 25 30

Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu
35 40 45

Phe Ile Met Arg Cys Gly Glu Ala Val Glu
50 55

<210> 55
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F and G from human KIAA0716

<400> 55
Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
1 5 10 15

Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu
20 25 30

Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met
35 40 45

Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala
50 55 60

<210> 56
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F and G from canonical DOCK2

<400> 56
Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
1 5 10 15

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
20 25 30

Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile
 35 40 45

Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
 50 55 60

<210> 57
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK3

<400> 57
 Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
 1 5 10 15

Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn
 20 25 30

Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met
 35 40 45

Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala
 50 55 60

<210> 58
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK180

<400> 58
 Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1 5 10 15

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
 20 25 30

Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile
 35 40 45

Ala Trp Gln Ile Pro Phe Leu Ala Glu Gly Ile Arg
 50 55 60

<210> 59
 <211> 4144
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human CLASP-3 cDNA

<220>
<221> CDS
<222> (197)..(3610)
<223> human CLASP-3

<400> 59
acgagtaaat cgttctcgaa gccttagtaa tagcaatcca gatatatctg ggactcccac 60
gtcaccagat gatgaagttc gatcaatcat cggagtaag ggttagatc gctccaattc 120
ctgggttaac actggtggtc caaaaagctgc cccatgggaa tccaaaccca gtccaaagtgc 180
agaatcaaca caggct atg gat cga agt tgt aat cgt atg tct tcg cac aca 232
Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr
1 5 10
gag acg tca agt ttc tta caa aca tta acg gga cgc tta cca act aaa 280
Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys
15 20 25
aag ctt ttt cac gag gag ctg gct ttg cag tgg gtt gtt tgc agt ggc 328
Lys Leu Phe His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly
30 35 40
agc gtt cgg gaa tca gct ttg caa caa gcc tgg ttc ttt ttt gaa tta 376
Ser Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu
45 50 55 60
atg gta aag agc atg gtg cac cat tta tac ttt aat gat aaa ctt gag 424
Met Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu
65 70 75
gct cca agg aaa agt cgt ttt cca gaa cgt ttc atg gat gac att gca 472
Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala
80 85 90
gct ctt gtc agc acg att gct agt gat ata gtt tca cga ttt cag aag 520
Ala Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys
95 100 105
gac aca gaa atg gtt gag aga ctc aat aca agc ctt gca ttc ttt ctc 568
Asp Thr Glu Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu
110 115 120
aat gat ctg ttg tct gtt atg gac aga gga ttt gtt ttt agc ctt ata 616
Asn Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile
125 130 135 140
aag tcc tgc tat aaa cag gtg tct tca aag ctt tac tca tta ccg aat 664
Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn
145 150 155
ccc agt gtt ctg gtg tcc ttg agg ctg gat ttt cta cga atc atc tgc 712
Pro Ser Val Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys
160 165 170
agt cat gag cac tat gtt aca tta aac tta ccc tgc agc tta ctt act 760
Ser His Glu His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr
175 180 185

cca cct gca tct cca tca cct tct gtt tct tct gca aca tct cag agt		808	
Pro Pro Ala Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser			
190	195	200	
tct gga ttt tct acg aat gta caa gac caa aag att gca aat atg ttt		856	
Ser Gly Phe Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe			
205	210	215	220
gaa tta tcc gtg cct ttc cgc caa cag cat tat ttg gca gga ctt gtg		904	
Glu Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val			
225	230	235	
tta aca gag ctg gct gtc att tta gac cct gat gct gaa gga ctg ttt		952	
Leu Thr Glu Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe			
240	245	250	
gga ttg cat aag aaa gtc atc aat atg gta cac aat tta ctc tcc agt		1000	
Gly Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser			
255	260	265	
cac gac tca gac ccg cgg tac tct gac cct cag ata aag gct cga gtg		1048	
His Asp Ser Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val			
270	275	280	
gcc atg ttg tat cta cct ctg att ggt att atc atg gaa act gta cct		1096	
Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro			
285	290	295	300
cag ctg tat gat ttt aca gaa act cac aat caa cga gga aga cca att		1144	
Gln Leu Tyr Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile			
305	310	315	
tgt ata gcc act gat gat tat gaa agt gag agc gga agt atg ata agc		1192	
Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser			
320	325	330	
cag acc gtt gcc atg gca atc gca ggg aca tcg gtc cct caa cta aca		1240	
Gln Thr Val Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr			
335	340	345	
agg cct ggc agt ttc ctc acg tca acg agt ggc agg caa cac act		1288	
Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr			
350	355	360	
acc ttt tca gca gaa tca agt cga agc ctt ttg atc tgt cta ctt tgg		1336	
Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp			
365	370	375	380
gtt ctc aaa aat gca gat gaa aca gtt cta cag aag tgg ttt aca gat		1384	
Val Leu Lys Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp			
385	390	395	
ctc tca gtc ttg cag cta aac ccg cta tta gat ctg ctt tat ctc tgt		1432	
Leu Ser Val Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys			
400	405	410	
gtg tct tgc ttt gag tat aaa ggg aaa aaa gtg ttt gaa cga atg aat		1480	
Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn			
415	420	425	

agc ttg acc ttt aag aaa tca aaa gac atg aga gca aag ctt gaa gaa		1528	
Ser Leu Thr Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu			
430	435	440	
gct att ctt ggg agc ata ggt gcc agg caa gaa atg gta cg ^g cga agc		1576	
Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser			
445	450	455	460
cga gga cag ctc gag aga agc cca tct gga agt gcc ttt gga agt caa		1624	
Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln			
465	470	475	
gaa aat ttg agg tgg agg aaa gat atg act cac tgg cgt caa aac aca		1672	
Glu Asn Leu Arg Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr			
480	485	490	
gag aag ctt gac aaa tca aga gca gag att gaa cac gaa gca ctg att		1720	
Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile			
495	500	505	
gat gga aac ctg gct aca gaa gca aac cta atc att tta gat aca tta		1768	
Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu			
510	515	520	
gag att gtt gtt cag acc gtt tct gta acg gaa tcc aaa gag agc att		1816	
Glu Ile Val Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile			
525	530	535	540
ctt ggt gga gtg cta aaa gtg cta cta cac agc atg gcc tgt aac caa		1864	
Leu Gly Gly Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln			
545	550	555	
agt gca gtt tat cta caa cac tgt ttt gct aca cag aga gcc ttg gtt		1912	
Ser Ala Val Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val			
560	565	570	
tca aag ttt cct gaa ctc tta ttt gaa gaa gag aca gag cag tgt gct		1960	
Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala			
575	580	585	
gat tta tgc ctc agg ctt ctc cga cac tgt agc agt agc atc ggt aca		2008	
Asp Leu Cys Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr			
590	595	600	
ata cgg tca cac ccc agt gcc tcc ctt tac cta cta atg agg caa aac		2056	
Ile Arg Ser His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn			
605	610	615	620
ttt gag att ggg aat aac ttt gcc agg gtt aaa atg cag gta cca atg		2104	
Phe Glu Ile Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met			
625	630	635	
tca cta tcc tcc ttg gtg ggc aca tct cag aat ttt aat gaa gaa ttc		2152	
Ser Leu Ser Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe			
640	645	650	
tta aga cgt tct cta aag act ata ttg aca tat gct gaa gaa gat ctg		2200	
Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu			
655	660	665	

gaa ttg agg gaa aca aca ttt cct gat cag gtc cag gat ctg gtt ttc		2248	
Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe			
670	675	680	
aat ctc cat atg att ctt tct gat act gtg aaa atg aag gaa cac cag		2296	
Asn Leu His Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln			
685	690	695	700
gag gat cct gaa atg ttg att gat cta atg tac aga att gcc aag ggt		2344	
Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly			
705	710	715	
tac cag acc tct cca gat ctg cga ttg acc tgg ttg cag aac atg gca		2392	
Tyr Gln Thr Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala			
720	725	730	
ggc aag cac tca gaa cga agc aat cat gct gaa gct gca cag tgt cta		2440	
Gly Lys His Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu			
735	740	745	
gtc cac tca gca gca ctt gtt gct gaa tat ttg agc atg ctg gag gac		2488	
Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp			
750	755	760	
cgg aaa tat ctt cct gtg gga tgt gta aca ttt cag aat att tca tct		2536	
Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser			
765	770	775	780
aat gtt tta gaa gaa tct gcg gtc tca gat gat gtg gta tct cca gat		2584	
Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp			
785	790	795	
gaa gaa ggt atc tgc tct gga aaa tac ttt act gag tca gga ctt gtg		2632	
Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val			
800	805	810	
gga tta ctg gaa caa gca gct gct tcc ttc tct atg gct ggc atg tat		2680	
Gly Leu Leu Glu Gln Ala Ala Ser Phe Ser Met Ala Gly Met Tyr			
815	820	825	
gaa gca gtt aat gaa gtt tac aaa gta ctt att cct att cat gaa gct		2728	
Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala			
830	835	840	
aat cgg gat gca aag aaa cta tcc aca att cat ggt aaa ctt caa gaa		2776	
Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu			
845	850	855	860
gca ttc agc aaa att gtt cat cag agt act ggc tgg gag cgg atg ttt		2824	
Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe			
865	870	875	
ggc acc tat ttt cgt gtt ggt ttt tat gga acc aag ttc ggg gat ttg		2872	
Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu			
880	885	890	
gat gaa caa gaa ttt gtt tac aag gag cct gca ata acc aaa ctt gca		2920	
Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala			
895	900	905	

gag ata tct cac aga ttg gag gga ttt tac gga gaa aga ttt gga gag		2968	
Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu			
910	915	920	
gat gtg gtt gaa gta atc aaa gac tct aat cct gta gac aag tgt aaa		3016	
Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys			
925	930	935	940
tta gat cct aac aag gca tat att cag att acc tat gtg gag cca tac		3064	
Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr			
945	950	955	
ttt gac aca tat gag atg aag gac aga atc acc tat ttc gac aaa aat		3112	
Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn			
960	965	970	
tac aat ctt cgt cga ttc atg tac tgt aca ccc ttt act tta gat ggc		3160	
Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly			
975	980	985	
cgt gcc cat ggg gaa ctt cat gaa caa ttc aaa agg aag acc att ctg		3208	
Arg Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu			
990	995	1000	
act acg tct cat gcc ttt cct tat att aaa aca agg gtc aat gtc act		3256	
Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr			
1005	1010	1015	1020
cat aaa gaa gag atc atc tta aca cca att gaa gtt gct att gag gac		3304	
His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp			
1025	1030	1035	
atg cag'aaa aag aca cag gag ttg gca ttt gca aca cat cag gat ccc		3352	
Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro			
1040	1045	1050	
gca gac ccc aaa atg ctt cag atg gta ctc cag gga tct gta ggc acc		3400	
Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr			
1055	1060	1065	
aca gtg aat cag ggg cct ttg gaa gtt gcc cag gtt ttt ctg tct gaa		3448	
Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu			
1070	1075	1080	
ata cct agt gac cca aag ctc ttc aga cat cat aat aaa ctg cga ctc		3496	
Ile Pro Ser Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu			
1085	1090	1095	1100
tgc ttt aaa gat ttt act aaa agg tgt gaa gat gcc tta aga aaa aat		3544	
Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn			
1105	1110	1115	
aag agc tta att ggg ccg gtt caa aag gag tat caa agg gaa ttg ggg		3592	
Lys Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly			
1120	1125	1130	
aaa cta tct tcg cct taa agaggcccta cagccctaga tcacagaaag		3640	
Lys Leu Ser Ser Pro			
1135			
tccctcagtt atccaagcca gtattgcttg tccccctgcc a cagagattcc ttcagtcgaa	3700		

ttagctttcg caaaatggat ctctaaactg aatgcacttg ttttattcat ctgcaaagag 3760
ccatgtattc aacatcgagt gtgaaaagat ctattggaaa ccaacatgga atgaaattct 3820
ggaaattatt attcattgaa gaatgcagtg gccaaagaaaa tatcaaatgt agattgttaa 3880
cgcttgagaa tcatggctat ggtttctaattt gttcgggtaa caagctgtta tcttttaaga 3940
catttaatg actcaaaggta acactataca ttaccattttt accattttt tagattcatt 4000
aaaaatttat tcactttaag ttcgtatccc ttaatttata tcaccattta tagattcatt 4060
ttggaccat tttaaatgta gtaatgctta tttaaaaggt actaaaaaat atgtgaatgt 4120
ttacctcgta cgcccgaggc cctc 4144

<210> 60

<211> 1137

<212> PRT

<213> Homo sapiens

<223> human CLASP-3 cDNA

<400> 60

Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu Thr Ser Ser
1 5 10 15

Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys Leu Phe His
20 25 30

Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser Val Arg Glu
35 40 45

Ser Ala Leu Gln Gln Ala Trp Phe Phe Glu Leu Met Val Lys Ser
50 55 60

Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys
65 70 75 80

Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala Leu Val Ser
85 90 95

Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp Thr Glu Met
100 105 110

Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu
115 120 125

Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr
130 135 140

Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu
145 150 155 160

Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser His Glu His
165 170 175

Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser
180 185 190

Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser
 195 200 205
 Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu Leu Ser Val
 210 215 220
 Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu
 225 230 235 240
 Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly Leu His Lys
 245 250 255
 Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His Asp Ser Asp
 260 265 270
 Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala Met Leu Tyr
 275 280 285
 Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln Leu Tyr Asp
 290 295 300
 Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr
 305 310 315 320
 Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln Thr Val Ala
 325 330 335
 Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg Pro Gly Ser
 340 345 350
 Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr Phe Ser Ala
 355 360 365
 Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val Leu Lys Asn
 370 375 380
 Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu Ser Val Leu
 385 390 395 400
 Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe
 405 410 415
 Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser Leu Thr Phe
 420 425 430
 Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly
 435 440 445
 Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg Gly Gln Leu
 450 455 460
 Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg
 465 470 475 480
 Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu Lys Leu Asp
 485 490 495
 Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp Gly Asn Leu
 500 505 510

Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu Ile Val Val
 515 520 525
 Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu Gly Gly Val
 530 535 540
 Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser Ala Val Tyr
 545 550 555 560
 Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser Lys Phe Pro
 565 570 575
 Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu
 580 585 590
 Arg Leu Leu Arg His Cys Ser Ser Ile Gly Thr Ile Arg Ser His
 595 600 605
 Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile Gly
 610 615 620
 Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser Leu Ser Ser
 625 630 635 640
 Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser
 645 650 655
 Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu
 660 665 670
 Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn Leu His Met
 675 680 685
 Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu Asp Pro Glu
 690 695 700
 Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser
 705 710 715 720
 Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His Ser
 725 730 735
 Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val His Ser Ala
 740 745 750
 Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg Lys Tyr Leu
 755 760 765
 Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn Val Leu Glu
 770 775 780
 Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu Glu Gly Ile
 785 790 795 800
 Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu
 805 810 815
 Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu Ala Val Asn
 820 825 830

Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn Arg Asp Ala
 835 840 845
 Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala Phe Ser Lys
 850 855 860
 Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly Thr Tyr Phe
 865 870 875 880
 Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln Glu
 885 890 895
 Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His
 900 905 910
 Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu
 915 920 925
 Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn
 930 935 940
 Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr
 945 950 955 960
 Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu Arg
 965 970 975
 Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His Gly
 980 985 990
 Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser His
 995 1000 1005
 Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu Glu
 1010 1015 1020
 Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys Lys
 1025 1030 1035 1040
 Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro Lys
 1045 1050 1055
 Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
 1060 1065 1070
 Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
 1075 1080 1085
 Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
 1090 1095 1100
 Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu Ile
 1105 1110 1115 1120
 Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys Leu Ser Ser
 1125 1130 1135
 Pro

```

<210> 61
<211> 755
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 1.1
      sequence of bacterial artificial chromosome BAC8
      using primer C3S3

<220>
<221> modified_base
<222> (1)..(755)
<223> n = g, a, c or t

<400> 61
tttttgaat taatggtgag caaaaactga gcatgttctt taatatttt tctcttagtg 60
aacaattta tgctagctca tttgttacct tagaaatctt tttctgttgc acatcttaac 120
gctttccat gtgcctctaa gacaaaatta catgtgttac atctctaaat aaacactgtg 180
gacactcaac acagtttagg tggattaag agtgaggctc attttaactc ttatttctc 240
aggatgggt gcataagcta gctatattt caaagggaaac ttgtgataca ttctttgcta 300
gtcattatac atgaagtgtt taatgacagt attgttagatt ttataccaaa gatggaaaga 360
gctttataga taccactgc tattgttatg gctagtaaac ccttagggaa atgccagtt 420
caatcaataa aaaaacaaca gtctggctgg gtgcagtggc tcacacctgt aatctcagca 480
ctttagaagg ccgaggcagg agatcactt gagatcagga gtttgagacc cagcctggc 540
aacatagcaa gagcccata ntacccaaaa aaaattttt tttaaattaa gctaaaaccc 600
tggnnngcca caaaacctgt agttcccatc tactttggaa aggcttgaag gangggaggg 660
cttgctttga gccccaagaa ngttcaaagg ctngcngnca gttntgatt cnacacntgc 720
aactcccgca ttgggtnaac aaaanccaag gaanc 755

<210> 62
<211> 798
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 1.2
      sequence of bacterial artificial chromosome BAC9
      using primer C3S3

<220>
<221> modified_base
<222> (1)..(798)
<223> n = g, a, c or t

<400> 62
aattaatggt gagaaaaac tgagcatgtt cttaatatt tttctctta gtgaacaatt 60
ttatgctagc tcatttgtt ccttagaaat cttttctgt tgcacatctt aacgctttc 120
catgtgcctc taagacaaaa ttacatgtgt tacatctcta aataaacact gtggacactc 180
aacacagtt aggtgaaatt aagagtgagg ctcattttaa ctcttatttt ctcagggatg 240
gttgcataag ctagctatat ttcaaagga aacttgtgat acattcttg ctagtcatta 300
tacatgaagt gtataatgac agtattgttag attttatacc aaagatggaa agagctttat 360
agatacccac tgctattgtt ntggctagta aacccttang gaaatgccag ttncaatcaa 420
taaaaaaaca acagtactgg ctgggtgcag tggcttacac ctgtaatctc agcactttat 480
aaggccccnag gcngggaggt cacttnagat ccaggagttt gagaccagcc tgggcaacat 540
ancaagagcc cattatctac caaaaaantt tttttttaa aattaagcta aacnctgggt 600
ggncacaaacc tggtnngnttc cnatntncct ttggaaaagc ttangaaggg gagggcttnc 660
tttgganccc caaaaagtn aaagggnntg cagtcagcct tttnaatcac ccnnnggncc 720
tntcgcattt ggattnccaa nangccaang naaccccgnt cntntttaa aaaantntt 780
taaagnannt ttnttngn 798

```

```

<210> 63
<211> 656
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 2.1
      sequence of bacterial artificial chromosome BAC8
      using primer HC3AS7

<220>
<221> modified_base
<222> (1)..(656)
<223> n = g, a, c or t

<400> 63
tcttnngaa aaagattana ttattaattc tatgatatat taacaataca canctctaac 60
actggacta ttttaaaat atggcatgta attaataga tgactgaaat atttagctt 120
ctcaaattt tttaaagtt ccctacaatg tttgtattt gctaaaata aaataaaaaa 180
accaccatat tacttcaga aaattatgct agctaacaat aggacaaaaaa attctgtgta 240
tgtcaacaaa aaaaattcaa ccttaaattt ttttttcc ataaaaaaca gggctacttg 300
cccaggtgag angtgctgcc gtatgagctc ctcgntagat tgcgcnccg gantgtcggn 360
ccctncgtt aatataacgg cgtgngcntg taccgcaggc tntgcttaggt cgtgnccca 420
agatatcntn tntancatan tagacgntgg ngnagnntgc atgtggcntn attntngcaa 480
ttgttnacaat cctagtntgt acntnanagn tcngccnctg tganntcggt gtatagtcng 540
ngcncgctt gnttctgatg ctgagagcan tnnccnnactn tttnncnncc atcttncnn 600
ttnnnnnccc cnnttnnat nnttnnnntn ncnnnnnnat ntntnaannn accncc 656

<210> 64
<211> 967
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 2.2
      sequence of bacterial artificial chromosome BAC9
      using primer HC3AS7

<220>
<221> modified_base
<222> (1)..(967)
<223> n = g, a, c or t

<400> 64
gcgctnccnn ntnnttatac ttctgaaaag actnatatna ttctatgatt ataacattac 60
acactctaac actggacttn ttaaatatgg atgtaattaa tagatgactg aatattttag 120
cttctcaaat atntttaang tccctacaat gtttgnatnt gctaaaata aaataaaaaa 180
ccccatatta ctttcagaaa antatgctag ctaacaatag gacaaaaaaa ttctgtgtat 240
gcaacaaaaaa aaaaattcaac cttnaatctt ctttttttc caataaaaaa cagggctact 300
ctgccacagg ctggagtcag tggctgatac agctactgca gctcactccg ggctatgtga 360
ttgcctgcct aagcctcnga gtagtaggct caggtgccac tacatgccag taatctaaaa 420
tttatagaga cagggctgct gtgtgnccag gctggctaac tccggctaa gcgttcttgc 480
ctngctctaa atgtggata cagnatgtat catncatcag ccaaaaagtt aattaanttc 540
cagatnanta tttgcataa agctccaatn tagcttgaag tagaacctgc tcnttggcta 600
gantatcccg nntgttatgg atcatattan gcnnntgtga tgccgaatgg natctattcc 660
gggagacana ttactatngg atganagcan atngccnnna tgcttntttg taacgctnna 720
nntaagaacn ttctngacat cgtcatagnt cgaagtnntn ngcganttga tactaanttc 780
atgntangcc natgactntn gtgattnntg antgnctggg agaacctacn tncccccnc 840
nnatannctn cacccctac tacttnncn ntcnctct anttctactc cacnttatta 900
tcctcnnccct tcncatcncc ccatcnatn tcnacgccnc nanacttanc nttnatncac 960

```

<210> 65
<211> 722
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 3.1
sequence of bacterial artificial chromosome BAC8
using primer C3AS4

<220>
<221> modified_base
<222> (1)..(722)
<223> n = g, a, c or t

<400> 65
taatgtacat agtgcgtcatg actgcagatg attcgttagaa aatccagcct caaggacacc 60
agaacactgg gattcggtaa tgagtaaagc tttgaagaca ccttgtaagc aatgcataag 120
taagagaaca ccaattgaat ctattatttc tttaatacta ataccagaat ggcaaattag 180
aattaaagag atagtacttg gtatccagtt tgggtttgt ggcttaagta gcagtatcac 240
cttttccag agttactgct aaaattaaaa attttaaact atcaggttt ctgtataaac 300
atatttact aacctaaaag ccacattctt gtatttccaa tatagcatca atatttctac 360
ttctcataaa acagggaaaaa cgtatatcac caaaaataac ttcttattac ttccttctta 420
aaagaaatta tcaattctt ttatagcact ttgtgcttac ctgtatttat aatttgtctg 480
ttttctcagc aacatcataa gctacttgag gagacatact ataaactgat ttaacagctt 540
tagtgtccct acagcttagc tcaatgtttg acaaataatag gagatcaatg cttaaaggaa 600
taaaggccag gacaagttct ggttagcaaat agtccataaa aggtttggg ggaaaagggt 660
aaaaatggat acatatcggt gtngcaagnt tttccatgt ggggtgaggt gccccatgcc 720
tt 722

<210> 66
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 3.2
sequence of bacterial artificial chromosome BAC9
using primer C3AS4

<220>
<221> modified_base
<222> (1)..(783)
<223> n = g, a, c or t

<400> 66
taacatagtg ctctgactgc agatgattcg tagaaaatcc agcctcaagg acaccagaac 60
actgggattc ggtaatgagt aaagcttga agacaccttg taagcaatgc ataagtaaga 120
gaacaccaat tgaatctatt atttcttta tactaatacc agaatggcaa attagaatta 180
aagagatgt acttggtatc cagtttgggt tttgtggctt aagtagcagt atcacccttt 240
tccagaggtt ctgctaaaat taaaaatttt aaactatcag gtttactgta taaacatatt 300
tgactaacct aaaagccaca ttcttgtatt tccaatatag catcaatatt tctacttctc 360
ataaaaacagg gaaaacgtat ntcaccaaaa ataacttctt attacttcct tctaaaaag 420
aaattatcaa ttcttttat agcactttgt gcttaccctg natttataat ttgnctgntt 480
ttctcagcaa acatcataag ctacttgagg gagacatact attaaacctg attacagctt 540
ttangtgcc ctacagctt actcaatgtt ttgcaaaatn tnnggagatc aatggcttta 600
aaqaataaaa qancaaggac aagttntggg tngccatnag nacaataaaag gttttngggg 660

gaaaagggaa aaaatngatt ncatntcgng gtngcaagg tntttccat tgngggngg 720
agggcccat gccataantt ttaaccttc tttttngaa gaaattaaac nnttaaaggg 780
gtn 783

<210> 67
<211> 721
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 4.1
sequence of bacterial artificial chromosome BAC8
using primer HC3AS6

<220>
<221> modified_base
<222> (1)..(721)
<223> n = g, a, c or t

<400> 67
ccagtctgca atatgctgtg cgaagccgat atcaacttg catcttgtc ttgnncattcg 60
agaaaatcaga cttgtggaag taggagacag cttacagcgt gcacaagctc tcagcagagc 120
atatacgaat gaatctttc cagggagttt tttatatact acctgagcaa gccactttag 180
ctttggcag gaacttntgg atgttataag taatacttat atgaataata tgaaattaat 240
atttacttct ttacantct tctctttcc ttatcttagc ctttatcccc ttgtggaaaa 300
gacactatca atgctagatn ctcccagnc agagaattat gcagggttgg tcagagaatc 360
gacacagaca tggttacaga ttcttcttga aatacatatt gtgcacgagt tttttacant 420
atctcaattt agatctcaga cagcatntng actagngggt ctaggacata gatacatntt 480
tgngaacttc tatagaanaa cntntgcntt aaaaaggagc ttgttngana ngaatnnnct 540
gngaagggcc cgatacgana atttgacttc ggngaaaaatt nnnggattnn tacaaanttc 600
taggnggcac ctnaaaaang nntgggnacn ttggnggcgg aaaaaaaaaagcc cttcnnttag 660
ntntccnngaa aatggaaaaag tnccaanttc cnaaaaaaaaan gggctttgtt nnctncnan 720
a 721

<210> 68
<211> 921
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 4.2
sequence of bacterial artificial chromosome BAC9
using primer HC3AS6

<220>
<221> modified_base
<222> (1)..(921)
<223> n = g, a, c or t

<400> 68
gacgccagct ctgtacacag tctgcaatat gctgtgcggg aggccgatcatcaactattgc 60
atctttgtct nncatcgag aaatcagact ctgtggaagn aggccgacaa gactatacag 120
cntgcacana gcatctcagc aggcatataa gaatgaanc tttccaggaa gttattttata 180
tactacctga gcaagnactt caacttnggc aggaacttgt ggatgntt aagtataactt 240
atatacgtttaa natngaaatt aatatttaat tctttactt cttctcttt ctttatctta 300
gcctttatcc cctcgtgaaa aagagcacta atcaatgcta ttnctnccaa gncaggaatt 360
tatagcaggt tggtcgagaa tcgacacgac atgtttagt antcatctt aatacatnat 420
tgtgcacgag tntttactc tatctcaaaa tatagatctc agatcgtcta tngantatgn 480
ggttcttagga catgattaca ttttngggaa acttccatag aataaacntn tacctnaaaa 540

nangagcctg ttngaaatng aatctactnc taaagggcna gtnccanatt ttacttccgc 600
ganatntcng gatgttacaa gtctaggggg ncttagnac gttnatntt tgancggaaa 660
aaagcccttc tannggtcnc ctaatggaag cgccaattcc naanaaggnc tgtgttntn 720
gacatttacc ngnccntt ctaatcaaac ntnctttct nnnancnca ncncnnncct 780
atannctat cnctcnctn nnctcntcac tctcnnnct ntcttccntt ctnactntn 840
nnntcnctnn natnnncttc tcnnatccnt ctcannnnt cannctccct acnntncn 900
tnnttaccatc tncnccnncc t 921

<210> 69
<211> 628
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 5.1
sequence of bacterial artificial chromosome BAC8
using primer C3S6

<220>
<221> modified_base
<222> (1)..(628)
<223> n = g, a, c or t

<400> 69
gtatgatccg ccagaccgct gccatggcaa tnntagggac atcggtccct caactaacaa 60
ggcctggcag tttcctnctc acgtcaacgg tcaaaaacaat cttctacag aattttttt 120
tctngaaaga caaatattta ctaggatatg cccttaaata tatgagatga ttgtatcagc 180
tgatgaaaaa gtgctcagtt ttatttatga aaatattaaa gttcccagaa tattaactgt 240
cttctcccaa acagtttaa aaaatgatta cctcaagggtt tatggaaaaa agccccgtat 300
tctgcattca gaatttgaa aattgcctca ttatagatag ccatntctt tttttnttt 360
tttatnctt caagtcttag ggnacatgtg cacaacatgc agntagttt catatgtata 420
catgtgccat gttgggtgtgc tgcacccann aacccgcaat ttaacattttt gtntatctcc 480
aaatgctatc ctttcacccct tccccatnc cacaacaagg ccccgccnt tgngatgttc 540
cccttcctgt gcccactgtg tntcacattn cncttccn cccttantnn ngtcagaac 600
ntngccngtn gccctntntt tttnnccc 628

<210> 70
<211> 953
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 5.2
sequence of bacterial artificial chromosome BAC9
using primer C3S6

<220>
<221> modified_base
<222> (1)..(953)
<223> n = g, a, c or t

<400> 70
ccnctgatga ttatgaaagt gagagcggaa gtatgataag ccagaccgtt gccatggcaa 60
tcgcaggac atcggtccct caactaacaa ggcctggcag tttcctcctc acgtcaacgg 120
taaaaacaat cttctacag aattttttt tcttagaaaga caaatattta ctaggatatg 180
cccttaaata tatgagatga ttgtatcagc ttgtatgaaa aagtgctcag gtttatttt 240
aaaaatatta aagttccaga atatttaact gtcttctccc aacagttta aaaaatgata 300
cctcaggtt atggggaaaa aagccccgtt ttctgtcatt cagaatttg gaaaattgn 360
ctcattatag atagttcatt ttctttttt ttttttttt ttatacnnntt aaagttttta 420

aggggnacca tgttgcacca aanattgcag gggtnnggtt accattatgg ttattnccat 480
tggtncccc antgttggg gngttggctt tgccacccccc cagngtaaaa ccnnccgntg 540
cgaattttta aaacaanttt tgggggttat tanttnnttc ccaaaaatng gcnttttnc 600
ccttncccc ccttcnccc nccnnttcc caacnnanca aggggcccccc cggtantgg 660
ggaaatagnt ttcccccct tnccctngnn gggccaattg tgggnnnct ccattggnn 720
tgcaaanttc ccccaccnt nattgttggt ggngaaacca tttcccgggg ggtttggggg 780
tttttttgg tccccnttgc ccaantaatt tttgcnttga anaaaaagaa tggggtttc 840
caaagcttt ngtcnccatt tgntccctt anggnncnt tngttcnct tnccanaang 900
ggccaatgtg aaacnnccct tcattttttt ttattgggn ttnccnttat ggn 953

<210> 71
<211> 683
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 6.1
sequence of bacterial artificial chromosome BAC8
using primer C3S7

<220>
<221> modified_base
<222> (1)..(683)
<223> n = g, a, c or t

<400> 71
ttcttggag cataggtgcc aggcaagaaa tggcacggcg aagccgagga cagctcggt 60
cgtacacaat agttctcct cctggtgaga atttcttcaa tttcctttag ttgtatattg 120
taatgatcat tggtagtact cttcaatgtc aatcctatgc tttttaaaaa gtgttttaag 180
tgtaactgtg aattaacttg aataatcatt tctctgcagt aataaaagtt agaattctga 240
tttaggtgag tcagcatacc gcccccccccc ccgtttctc tagaaaagtct tctctagaaa 300
acgttctcta gaaagtccctt tctagaaaaac tttctctaga aagtccttat gtgattaata 360
gcatccatcc tccctttta aatagacttt atttttgttag agcagttta agttcacagc 420
aaaagtgagc aaaggtacag agattccca tataccctt agtatgcgt 480
ttattaacat cccccatcaa gagtagtgca tttgttgtaa ctggtaacc tacattaaca 540
catcatcacc cagagtccgc agtttacatt agggatcatt catataacat ctattttac 600
ttttttttt ttagttgaga caagatttgc gctctgtcac ccaagctgga gtgcagtccg 660
ngtggattgt nggcttactg ncn 683

<210> 72
<211> 807
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 6.2
sequence of bacterial artificial chromosome BAC9
using primer C3S7

<220>
<221> modified_base
<222> (1)..(807)
<223> n = g, a, c or t

<400> 72
gtgccggcaa gaaatggtac ggcgaagccg aggacagctc ggtacgtaca caatagcttc 60
tcctcctgg tggaaattct tcaatttcct tgagttgtat attgtatga tcattgtgc 120
tagtcttcaa tgtcaatctt atgctttta aaaagtgttt taagtgtac tgngaattaa 180
cttgaataat catttctctg cagtaataaa agttagaatt ctgatttagg tgagtcagca 240

taccggcccc ccccccgtt tctctagaaa gtcttccta gaaaacgttc tctagaaagt 300
cctctctaga aaactttctc tagaaagtcc ttatgtgatt aatagcatcc atcctccctt 360
tttaaataag actttatTTt tgtagagcag ttttagttc acagcaaaag tgagcaaagg 420
gcagagattt cccatatacc ccttagtatg ctagcctcc cccattatta acatccccat 480
cagagtaagn gcatttggta taactggnga acctacaatt nacacattnt naccccacag 540
tcccgcgagg ttacatttt gggatcattc ccctantaac acctattttt ttactttttt 600
tttttttag gttgagacaa gaattttcggtt cttcttgtt acccccaac tnggttagtag 660
ncnnaccgtc gngnaatttn tggggtttn tngngnncan tttgtgcnnnt cnncnnncn 720
ccnaaagaan tttttttca ccctttttt tccccnaan anannancct tccccttgg 780
ggangctggg gacttccnca gnggngg 807

<210> 73
<211> 721
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 7.1
sequence of bacterial artificial chromosome BAC8
using primer C3S8

<220>
<221> modified_base
<222> (1)..(721)
<223> n = g, a, c or t

<400> 73
caaagtgcag tttatctcaa cactgttttg ctcacagaga gccttggtt caaaggtagg 60
ttatTTgtt cctgcagtgt tgcagactt tgTTTTTTt attaacattt tctaagatca 120
tttgacacat tcattggta atatatgtt taatatatta atgaatatgtt gtagttaaaa 180
tttaaataat aacctaagac ccttaattct tcttgcctc tctactgctg cctgcctttt 240
agaatttttca atttattcga atcacctta accagttctg gtttggaaaaa cagtaacttg 300
gatgtggaga agggcctgaa attaatagcc aatcttaat atggggcttc tcttgTTTc 360
tcttcacttg gttctgttt tataaaaaac tcaatttata aagaattcaa tatataagca 420
attcaaccca ctgaaattat ttatgtga atggaaaaaaga aggtatgtgt ttgttcaact 480
gctttaatg ttacttctt atattgttt tcccttagaa atatgtatat tcttaaattt 540
tgaaggtgc tatttcattt taatcatcct agaggatgga atgcanagat gttggatgaa 600
aataacttac gtattttttt gtaataaata taagaattca tatatgggtt attacctaag 660
tggTTTatg cacattctga tagaaagctt caccaacaat ccctgntng atatattttt 720
t 721

<210> 74
<211> 836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 7.2
sequence of bacterial artificial chromosome BAC9
using primer C3S8

<220>
<221> modified_base
<222> (1)..(836)
<223> n = g, a, c or t

<400> 74
aagtcaGTTt atctacaaca ctgtttgct acacagagag ccttggttcc aaaggtaggt 60
tattttgtac ctgcagtgtt gtcagactttt gttttttta ttaacattgt ctaagatcat 120

ttgacacatt cattggtaa tataatgtg aatatattaa tgaatatgtg tagttaaat 180
ttaaataata acctaagacc ctaattctt ctgcctct ctactgctgc ctgccttta 240
gaattttca ttatcgaa tcaccttaa ccagttctgg tttgaaaaac agtaacttgg 300
atgtggagaa ggcctgaaa ttaatagcca atcttaataa tggggcttct cttgnnttct 360
cttcacttgg ttctgtttt ataaaaaact caatttataa agaattcaat atataagcca 420
ttcaccact gaaattattt tatgatgaat gaaaaagaaa ggtatgtgt tgttcacctg 480
ctttaaatg ngacntcnta atattttgn tttccctta agaaaatatg tataatcctt 540
aaaanttng aaaggangc tantttcatt ttttnaatca atcctaanaag ggattggaa 600
atgcncaaga tttttgatt gaaaaanaac cttancnat ttaatttttgn gnataaaaa 660
taattagnaa ttccntatta tgntnagaat tacctaaagt ggttttatt gcccatttc 720
nttgatatgn aaagccttc accaaccaaa ttccccttg nnaggaatat tatttttgn 780
nggcctcnt ntttgtggg ntggaagnaa aaaccttgc tccaaagggt cccnc 836

<210> 75
<211> 678
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 8.1
sequence of bacterial artificial chromosome BAC8
using primer C3S10

<220>
<221> modified_base
<222> (1)..(678)
<223> n = g, a, c or t

<400> 75
agtcttagtc ctcagcagca cttgttgctg aatattttag catgctggag gaccggaaat 60
atcttcctgt gggatgtgta acatttcagg taggaatctt ccagatgtac attaaatcaa 120
ggtatatctt ttttggttt tagctttct cactgggtt tagattttt tagtttataa 180
ggaaagctta aagacttaag ccaatgcttc acaaggtgaa ttaacatttc acagtgattg 240
tcattaatac atttttaagg agtacttctt gttgattctc tttccacagt ttcttacctc 300
tgaattatca gcactatgct tatttattct ctttggctt actgnctgn aatcccgta 360
catactttaa catctatgga aatgtattac tgataatcag aattcagtag aaattcttaa 420
ttggctttta cttcacatag cagatataacc aacattctt attccctaca taaaatatta 480
agattatttt atgactaata cccatgactc acagatgagt ttgccctcta gttagggtcat 540
aattctgacc cactagttga attctctgct taccaagagn caggtatgct tgcttttct 600
tcaaaacctg ttaaatagta ggnttgggaa tatntaaaa attaggtaaa tggtatatct 660
tctggtgaa ancagaan 678

<210> 76
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 8.2
sequence of bacterial artificial chromosome BAC9
using primer C3S10

<220>
<221> modified_base
<222> (1)..(825)
<223> n = g, a, c or t

<400> 76
cagcagcact tggtgctgaa tatttgagca tgctggagga ccggaaatat cttcctgtgg 60

gatgtgtaac atttcaggta ggaatcttcc agatgtacat taaatcaagg tataatcttt 120
tttggttta gctttctca ctgggttta gatttttta gtttataagg aaagcttaaa 180
gacttaagcc aatgcttcac aaggtaatt aacatttcac agtgattgtc attaatacat 240
tttaaggag tacttcttgc tgattcttctt tccacagttt cttacctctg aattatcagc 300
actatgctta tttattctct ttgtcttac tgccttgtaa tccgttacat actttaacat 360
ctatggaaat gtattactga taatcagaat tcagtagaaa ttcttaattt gcttnntact 420
tcacatagca gatntaccaa cattctctat tccctacata aaatattagg attatTTT 480
gactaatacc atgactcaca gattgagttt gccctctant agggtnncata atttctgacc 540
cactagtga attctctgt tacccaaagt canttatgcc tttgctttt cttcaaaaacc 600
ctgnntaatt aggnacggct ttggagataa tttataaaaaa atttcaagct naaantggnt 660
tattattcnt tccnnggttg aaaaaaccca ggaattggca caaannaana aaaagnttat 720
tccnngtttc ttncggnaa aaaaacccaa aaatcttnga aattgtttt taccaaaaan 780
gacctccncn gggaaaaagg gntaaattt nttccntaaa aacnn 825

<210> 77
<211> 904
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 9.1
sequence of bacterial artificial chromosome BAC9
using primer C3S11

<220>
<221> modified_base
<222> (1)..(904)
<223> n = g, a, c or t

<400> 77
ttcctattca tgaagctaattt cgggatgcaa agaaactatc cacaattcat ggtttttttc 60
aagaagcatt cagcaaaattt gttcatcagg taatgattcc aatttcttagc ttcactataa 120
aggaaaaaaa ctgtctgaaa gcattaatgt tggtttgcac tgatgtcaaa ctagatcccg 180
tgaatgacc atttaatca gactacaaat gagcggtcaa aatgatagtt catggccaaa 240
gcaaagctca ttaacaataa aaatgaattt acctaaagta aatggtgatc atcataaact 300
ttctgcatac cttttttttt ttcatttttg aattattaat taagcaagtt tttaaaaatt 360
gtgattttctt gtttccaaag gnaagatcat aagtttggaa atctcattttt taaaaatttga 420
taccctattt ctttgctgn ggaaaantgg aagttttta atattttcaaa gttttttttt 480
aaaattnaaa tggattgtgg aaaacctttt aaatnaattt aaaaccttacc taaaatantt 540
tttttaatgg nccnngccan ctggAACCTT tttttttttt tccccttagga atggTTTAC 600
ccaaatccat tcccttttga ataatatttt tccctnaattt ncccaaaaaaa ntttttnttt 660
tttggggngg aaaaaatantt tggaaaattt aaaaaatggg ggtggggccn taaatgggg 720
tttttttaa atttcctaaa aaagggantt ttccatttac cttttaatcc tttttggng 780
gnttcnattt attggggaat cctncncttt tttntncncc ttaaaaaant tagggcctnc 840
caaaatttta aaccntttaa tttttaaaaa ngggaaagggn cccctttctt ngccccgggtt 900
gttt 904

<210> 78
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 10.1
sequence of bacterial artificial chromosome BAC8
using primer C3S12

```

<220>
<221> modified_base
<222> (1)..(681)
<223> n = g, a, c or t

<400> 78
tacagattgg aggtgaatgc tgtgggtgtt cataaaatgt catcttagt ttgtattctc 60
tctgatgatt agactttcag atccagatct aatcatttag taagccagat cttgccaat 120
aaactactcc gttagagaat aaggacttt aatagtaca ataatactct ttcaaattctt 180
ttatggcagc aataaaatag taatattgtc tatttttga gactatttc acacatattt 240
tagaaacccc tgtatccttc agaattactg cgacttaacg gagaatata tagtataatc 300
ccacatttt tgaaaaaaa caaagaatta agtagtagct aataattgaa ctagaaccag 360
aaccctaaga aatttctgac ccaagcatat tatctctttg gcttaactgg ttccaggtga 420
ggttcttta gaacgtaaaaa gcctgaaatc acaccttaaa aacacttcct ttaaccttta 480
taatttctta atttcacca taaatgattt cgtttatat ttactggggc taactagnat 540
tttctgntat agtattctt tccaaccttt ctctatttt tgtaactcaa agttagtgg 600
atggaccgga agcattgggg ttcacctggg agaatgggtt gnaatgcaga acccttagac 660
cccaccccaag cccctgtgaa a 681

<210> 79
<211> 879
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 10.2
      sequence of bacterial artificial chromosome BAC9
      using primer C3S12

<220>
<221> modified_base
<222> (1)..(879)
<223> n = g, a, c or t

<400> 79
cagatagtag gtgaatgctg tggtggttca taaaatgtca tcttttagttt gtattctctc 60
tgatgatttag actttcagat ccagatctaa tcatttagta agccagatct tgccaaataa 120
actactccgt tagagaataa ggacttttaa tagttacaat aatactctt caaatctttt 180
atggcagcaa taaaatagta atattgtcta tttttgaga ctatttcac acatatttta 240
gaaacccctg tatttcctcag aattactgcg acttaacgga gaaatataa gtataatccc 300
acattttgtt gaaaaagaca aagaattaag tagtagctaa taatttgaac tagaaccaga 360
accctaagaa atttctgacc caagcatatt atctctttgg cttaactggg tccagggngag 420
gtatctttag aacgttnaaag cctgaaatca caccttaaaa acacttnctt taacccttta 480
taanttnctt aattttcacc cataaaatng attgcngttt tatattttac ctngggncta 540
nacctnaggc aattttctg ggtcataagg gaaatttctt tttcccaaac cctttcttc 600
ttattttgtt gggncaccc ccaaaaggtg ntcngtggg gnttngggnc cccngaaag 660
gccatttggg ggnttcaccc ccgggggang atttggttt ggaaaatngt cnnaaaaacc 720
ttccnnaccc ccnncccccn ggcccccntg nnngaaatc caaaaggatc ttgnncnattt 780
tttanccaa angancnccc ccnagggngg gatttngtt atttccccaa naagangtaa 840
ggttnttggc cttnngggc nttgggtgtt tttntttnn 879

<210> 80
<211> 786
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 11.1
      sequence of bacterial artificial chromosome BAC9
      using primer HC3AS3

<220>
<221> modified_base
<222> (1)..(786)
<223> n = g, a, c or t

<400> 80
ctgangtgn gcaangccac tcctgtgtct tttctgcatt tcctcaatag caacttcaat 60
cggtgttaag atgatctgag tnanngagca tctgttanat cagngtactg actgaaaacta 120
tttaatgaac tttatgtata atcaactgaa attaganaaa aaaaagatca atngtaaact 180
tcatgtaca ataaaattcc aaacttggat tctaaatgaa nnaaaaanat caacctttaa 240
agaaaagctg ggggtgaata agggcttaga aaagangtan aaaatganga ctcaaaaatgg 300
taaagggtct aatatgnatg gataaggatg gacatatctt cgactctga gtgggttaca 360
tggcttgatg attgctact atgtgtgnca ttatggctac ctctcttttag gcattgcctgt 420
taantaggaa gctgaactan caaagnctct tngatgtatn antcctgccc ctnaagaagg 480
ggncgcntga nncaaattgtt ttgcnatgtn tctgctatna tngnaagnn tcctngantn 540
nttcnganana anctctcnan gagnctgtt tacatncggt cagncttct tgcacccct 600
gngcatctcc cgtanttcac cctcatttna ccntnattt ataannannn agcccacntn 660
ncctatagcc natcnacgcn nttcccnnta ntcantnnna gacaattttt tnnccccccc 720
tcctnnntcct tcctnnnttc cncccnncnn ccctntntct ntncnnncn cnnttcttan 780
cttnct                                         786

<210> 81
<211> 933
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ref 12.1
      sequence of bacterial artificial chromosome BAC9
      using primer C3S15

<220>
<221> modified_base
<222> (1)..(933)
<223> n = g, a, c or t

<400> 81
tgtaaaaaga tctattggaa aacaacatgg aatggaaattc tggaaatttat tattnattga 60
agaatgcagt ggccaagaaaa atatcaaattt tagattgtt acgcttgaga atcatggcta 120
tggtttctaa tggtctggta acaagctgtt atcttttaag acattttat gactcaaagg 180
tacactatac atttaccatt atttatacca tagcttaagg taaaaatttta ttcactttaa 240
gttcgtattt tttaattttt attaccattt atagattcat tttggaaacca ttttaaatgt 300
agtaatgctt attttaaagg tactattaaa tatgtaaatg tttacactaa ttttaccgag 360
tgggacttca aaatttttat tattgacaat ggctgagaac aattnaaggg tttgactcna 420
gaactanttc caaaccttagc agaataaaaa tcatagatag ccccaaatta atgagtttgg 480
gnaactgtnt caaagttttt ttccattttt atacccaaaa acagggaaattt tttagaattt 540
ccngaacctt taccttaaga naaaaaacccct tttgtgnntna aaaatntant nttaaaattc 600
ccggggggan taatcttaat naccccggtt gggccannnc ncccccattt aactttggaa 660
tttaaaaattt cttttttttt ncaaccccaa actgnantng ggtntttttn aaggaaaacc 720
tttccactng gaagttnnct ttttagggnc nancctncna naaannnnnn aanattttgg 780
agtcttcccc ttcnttnggg gggngnccca aaaaattttt aataaaaanc ccggggctcc 840
catnttagn attttttttt ttggcccccac actgtgttta ttaaancccc ncngctaaa 900
aattttnnn gaaaanacct naacccttctt nna                                         933

```

<210> 82
<211> 100
<212> DNA
<213> Homo sapiens

<220>
<223> exon 60270-20370

<400> 82
cgccgcagcc gccgcccgg tcgccgtcgc cgtagcagcc atggccgagc gcccgcctt 60
cgcccagaag atcagcaggt aaatatccgg cgtggggcgc 100

<210> 83
<211> 151
<212> DNA
<213> Homo sapiens

<220>
<223> exon 85360-85510

<400> 83
gttttgctt tcttcattgt agaacggtgg cagccgaagt taggaaggcag atctccggac 60
aatatagtgg ttctccccaa ctgctcaaaa accttaatat tggtggcaat atatcccatc 120
acaccacagt aagtaacgta ttcaaaaatat a 151

<210> 84
<211> 220
<212> DNA
<213> Homo sapiens

<220>
<223> exon 94500-94720

<400> 84
tcttatccca acttttaca aaggtgcccc ttaccgaagc agtagatcca gtggatttg 60
aagattacct cattactcat cctttggctg tggattctgg gccttacgg gatttgattg 120
aatttcctcc agatgatatt gaagttgtt atagtcctcg ggactgcaga actcttg 180
cagctgtacc tgaagaaagg taaggagaca ttgacttatt 220

<210> 85
<211> 111
<212> DNA
<213> Homo sapiens

<220>
<223> exon 94870-94980

<400> 85
tatttcctt tttaaaatag tgaaatggat ccacatgtta gagactgtat aagaagttat 60
acagaagact gggcaattgt catcagaaag taagttatat gtttattaca a 111

<210> 86
<211> 180
<212> DNA
<213> Homo sapiens

<220>
<223> exon 100110-100290

<400> 86
atttatttaa cttttttct ttaatagata tcataaattg ggaacaggat ttaatcccaa 60
tacatttagat aaacagaaag aaaggcaaaa aggttgcca aaacaagttt ttgaatctga 120
tgaagctcca gatggcaaca gctaccagga tgatcaagta atacttttat tcttaaataa 180

<210> 87
<211> 260
<212> DNA
<213> Homo sapiens

<220>
<223> exon 100340-100600

<400> 87
atatttaatg ttttgcata caggatgacc taaaaagacg ttcaatgtca atagatgata 60
ccccaaagggg tagctggcc tgtatctttgactt gaaattcactt cctgatgctt 120
tgcttcccaa ttacttgat cgaactccaa atgaagaaat agaccgtcag aatgatgacc 180
aaaggaaatc aaaccgtcac aaagaacttt ttgcttgca tccatcacca gatgaggtat 240
agatgtttgc atataaagaa 260

<210> 88
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<223> exon 100880-101020

<400> 88
ttttgggttt gctttcaat ttgttaggaag aaccaataga acggcttagt gttcctgata 60
tacccaaaga acattttgtt caaagacttc ttgtaaaaatg cttatcactc aagtgagttat 120
ttatttcttt tacttacaac t 141

<210> 89
<211> 111
<212> DNA
<213> Homo sapiens

<220>
<223> exon 112010-112120

<400> 89
tttttcttca taaaggttt gaaattgaaat tgaaccatt tttgcaagtt tggctttata 60
tgatgtcaag gaaaagaaaa aggttaagatt atataattt accatagttt a 111

<210> 90
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<223> exon 113680-113880

<400> 90
aagtttaaca tactaatatt ttttagattt cagaaaactt ttatggac cttaattctg 60
agcagatgaa agggttgtt cgtccacatg taccacctgc tgccattact accctggcaa 120
gatcagcaat ttttctatc acttacccctt cccaagatgt tttcttgta ataaagggtga 180
gaataatgtt aaatatattt g 201

<210> 91
<211> 140
<212> DNA
<213> Homo sapiens

<220>
<223> exon 115020-115160

<400> 91
ttaatcttaa cttttttgc ctttgacagc tagaaaaagt cctacagcaa ggagacattg 60
gagagtgtgc agaaccatat atgattttca aagaagcaga tgccaccaag gtggatgtt 120
atgcttctca tttccgccac 140

<210> 92
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<223> exon 117200-117410

<400> 92
atgtataaaag ttctgttttgc cagaataaaag aaaaactgga gaaactgaag agtcaagcag 60
atcagttttgc ccaaagactt gggaaatatc gcatgcctt tgctggact gcaatccatt 120
taatgaatat tgtagcagt gctggagtt tggaaagaga ttctacagaa gtggaaatca 180
gtactggagg taagagtgtt tcataaaaaa c 211

<210> 93
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<223> exon 123200-12396

<400> 93
aaaatgaatt tttttttaa ttctttgtt gaacgaaaag ggtcttggtc agagaggagg 60
aattcttagta ttgttggcag acgatcactt gaaaggacaa caagtggaga tgatgcttgt 120
aacatggcga gcttcgacc agctactctc acatgtacaa attttttaa gcaggtattt 180
ttctgtcatg taggaatttt 200

<210> 94
<211> 94
<212> DNA
<213> Homo sapiens

<220>
<223> next part of CLASP starting

<400> 94
gaaggagacc gcttaagtga tgaagatctc tacaaattcc ttgctgatat gagaaggcca 60

tcttctgtct tacggcgact aagacctatt acag

94

<210> 95

<211> 151

<212> DNA

<213> Homo sapiens

<220>

<223> exon 5560-5710

<400> 95

cttttcctc tattattgaa atcaggaagg agaccgctta agtgatgaag atctctacaa 60
attccttgct gatatgagaa ggccatcttc tgtcttacgg cgactaagac ctattacagg 120
tattaaaaaa ttttagtag aaatggttgc a 151

<210> 96

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<223> exon 6680-6900

<400> 96

ttacattgtt tttaatata taattgcag ctcagctcaa gatagacatt tctccgcac 60
ctgaaaatcc ccattattgc ctaactccgg agctgcttca agtgaagctt taccctgaca 120
gtagagttag acctaccaga gaaatcttag agttcccgc aagggatgtt tatgttccaa 180
acactactta caggtaagag atttaattt ggagaattct g 221

<210> 97

<211> 156

<212> DNA

<213> Homo sapiens

<220>

<223> exon 38920-39075

<400> 97

gtatTTacta tcATCTatac tgTTgCTTc acagaAATct tCTCTacata taccCTcaga 60
gtCTtaattt tgCCAAATCgt caaggTTctg ctagAAATat aacAGTgAAA gtCCAGTTa 120
tgtatggaga ggatCCAAGC aatGCCatGC cggtaa 156

<210> 98

<211> 2349

<212> DNA

<213> Homo sapiens

<220>

<223> putative promoter region for human CLASP-3,
genomic sequence upstream of human CLASP-3 5'
terminus

<400> 98

gtaagctgca gagtacatgc aaagtccTTT cagacacttt ggcaactagt gagtcATGta 60
tacAAAGAAC tattCAAAGC AAAATGTGGC cagttctcta agagAGTAGT gaaaAGATgt 120
ttggagaaca gagataAAGG catgcaACAT ctggCTGGGA gtgtgAGAGC agacaACCAA 180
ttcaggGACT atcaaACACC caggacaAGC ttaAGTACAG gatGAATAAT gacAGTAACA 240

gtgataataa taacaacagc tgacacacat cgtacttacc atgaaccagg ccctgttcta 300
 agaactttat attaatcaat tcaataaaatc ttcacaacac ccttcaagt agatataatt 360
 atttcctcc ttttagagat gaagttaagt agcttgctta aggttacaga gtaagaaaagt 420
 ggcaaaataa gtctgggttc ctatcacaga gggcttaaa agccaggtac agtgatagcc 480
 ttgacttaca gtctgtgagt acctggttca tcttcccaa tggactcaaa cattctgaga 540
 gcaggtctgt gtctagttca cttcgtgtt ttttagaaca cctaggtggg ctctatactt 600
 aggtagaagc caaatatctg tcctcttga atagactatc tttccctta gtaaacaagc 660
 atctgaaaac agtgtgttac tggagggcgc cttggcaaga gcctgtggta cttagctactc 720
 ctccagagggc tgaggcaaga ggattgctt agcctaggag ttttaggctg cagtgcccta 780
 tgcattccat gcttgagcaa cacaggggaa ttctgtctaa aataaataaa tcaataaataa 840
 aaagcagtgt gttactgcaa tgagcattgt tatataaata cacagtctc cacagaagtt 900
 acagcactag acaggaagtt atggatctga ctaattgagg cttcacctc tgactcagtg 960
 tgtgactctg gcaagtgacc taatggctcc aagctacaga tttccaatg gtaaaaagaga 1020
 ggaaaacagg tatccaacat attccaccag gacatactga gaatataata ataacaataa 1080
 ataaatacac atttaagtt ctgcataac ttaagagggaa aggtactaca agaaaccaag 1140
 atattttct tagtgtcacc ataatttcag tatcaacaga tatgcattag gagccaaata 1200
 ttcttagacat tatgggatta caacagaaca gatgaaaaca aatctctgct agtctctgtt 1260
 ttataggcta ttatggacaa ggtcagttc agtggtcaac acagagctt ttaacagaa 1320
 catcaaaatg ggggtgaacg ttagagctca cctggatttt atatatatat atatatatat 1380
 atatatatat atatatatat gtatgagaga cagagagaga tccaaaaggg gtaataataa 1440
 cgaaaaacaac tgcctcaaa gaaaagaacc ggctctgggt ttgagtcata gttggaaaggt 1500
 ttaccatctg tgcgacctgg ggccagtcac ttagctttc caagccaatt tcctccctc 1560
 taaaatagtg atagtaacga tctacttcaa agcgctcgtt cttgaaaaac ttaatccag 1620
 tggctggcta agcaccagaa gtcaactatt actattgtt tcgctgcagg agcaaggtat 1680
 tttctggctc tttctctata agaaaaacca ctgtttctcc agttaggctg cattcatgag 1740
 gccgaagcag aaacccaagt gcttaaaaaa gctcggagac cggtgctgca gaaacatgaa 1800
 cccagtcattc cagggctttg gttaaagcac agccccctcg gcaaagccc ccttcattt 1860
 cttcccttc catttcggga aagccaagct cccctacgc gttcggttat cttatattct 1920
 tgcctcgcca ggtcgctggc ctgtctctgg cttctctccg cgacctctcg gtcgtgcagg 1980
 ctccgcggca gcaagcggc tggggctggc gcctcgcttc ctcagcgctc cattctccc 2040
 ctggctccc gccggccgca gccgccttcc gcagccgggg ttcccgccgg gattgacgcg 2100
 ctgggggagg agcggtttct cggtgcgcgc ctctaaggaa cattacggca gggctcggtc 2160
 ctggctccgg cggccagccc cagcctccca ggtccggagc ccggactggc ggaggccgcg 2220
 agggagggag cacgagcgcg gaggcacgcg cccgcccgtc cgcacccggc cggccgcagc 2280
 cgccgcccggc gtcgcccgtcg ccgcagcagc catggccgag cgccgcccgtc tcgcccagaa 2340
 gatcagcag 2349

<210> 99
 <211> 2008
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-4

<400> 99
 Met Phe Pro Met Glu Asp Ile Ser Ile Ser Val Ile Gly Arg Gln Arg
 1 5 10 15

Arg Thr Val Gln Ser Thr Val Pro Glu Asp Ala Glu Lys Arg Ala Gln
 20 25 30

Ser Leu Phe Val Lys Glu Cys Ile Lys Thr Tyr Ser Thr Asp Trp His
 35 40 45

Val Val Asn Tyr Lys Tyr Glu Asp Phe Ser Gly Asp Phe Arg Met Leu
 50 55 60

Pro Cys Lys Ser Leu Arg Pro Glu Lys Ile Pro Asn His Val Phe Glu
 65 70 75 80

Ile	Asp	Glu	Asp	Cys	Glu	Lys	Asp	Glu	Asp	Ser	Ser	Ser	Leu	Cys	Ser
				85					90					95	
Gln	Lys	Gly	Gly	Val	Ile	Lys	Gln	Gly	Trp	Leu	His	Lys	Ala	Asn	Val
				100				105					110		
Asn	Ser	Thr	Ile	Thr	Val	Thr	Met	Lys	Val	Phe	Lys	Arg	Arg	Tyr	Phe
				115			120					125			
Tyr	Leu	Thr	Gln	Leu	Pro	Asp	Gly	Ser	Tyr	Ile	Leu	Asn	Ser	Tyr	Lys
				130			135				140				
Asp	Glu	Lys	Asn	Ser	Lys	Glu	Ser	Lys	Gly	Cys	Ile	Tyr	Leu	Asp	Ala
				145			150			155			160		
Cys	Ile	Asp	Val	Val	Gln	Cys	Pro	Lys	Met	Arg	Arg	His	Ala	Phe	Glu
				165				170					175		
Leu	Lys	Met	Leu	Asp	Lys	Tyr	Ser	His	Tyr	Leu	Ala	Ala	Glu	Thr	Glu
				180				185					190		
Gln	Glu	Met	Glu	Glu	Trp	Leu	Ile	Thr	Leu	Lys	Lys	Ile	Ile	Gln	Ile
				195			200					205			
Asn	Thr	Asp	Ser	Leu	Val	Gln	Glu	Lys	Glu	Thr	Val	Glu	Thr	Ala	
				210			215			220					
Gln	Asp	Asp	Glu	Thr	Ser	Ser	Gln	Gly	Lys	Ala	Glu	Asn	Ile	Met	Ala
				225			230			235			240		
Ser	Leu	Glu	Arg	Ser	Met	His	Pro	Glu	Leu	Met	Lys	Tyr	Gly	Arg	Glu
				245				250				255			
Thr	Glu	Gln	Leu	Asn	Lys	Leu	Ser	Arg	Gly	Asp	Gly	Arg	Gln	Asn	Leu
				260				265				270			
Phe	Ser	Phe	Asp	Ser	Glu	Val	Gln	Arg	Leu	Asp	Phe	Ser	Gly	Ile	Glu
				275			280			285					
Pro	Asp	Ile	Lys	Pro	Phe	Glu	Glu	Lys	Cys	Asn	Lys	Arg	Phe	Leu	Val
				290			295			300					
Asn	Cys	His	Asp	Leu	Thr	Phe	Asn	Ile	Leu	Gly	Gln	Ile	Gly	Asp	Asn
				305				310			315			320	
Ala	Lys	Gly	Pro	Pro	Thr	Asn	Val	Glu	Pro	Phe	Phe	Ile	Asn	Leu	Ala
				325					330				335		
Leu	Phe	Asp	Val	Lys	Asn	Asn	Cys	Lys	Ile	Ser	Ala	Asp	Phe	His	Val
				340				345					350		
Asp	Leu	Asn	Pro	Pro	Ser	Val	Arg	Glu	Met	Leu	Trp	Gly	Ser	Ser	Thr
				355			360				365				
Gln	Leu	Ala	Ser	Asp	Gly	Ser	Pro	Lys	Gly	Ser	Ser	Pro	Glu	Ser	Tyr
				370			375			380					
Ile	His	Gly	Ile	Ala	Glu	Ser	Gln	Leu	Arg	Tyr	Ile	Gln	Gln	Gly	Ile
				385			390			395			400		

Phe Ser Val Thr Asn Pro His Pro Glu Ile Phe Leu Val Ala Arg Ile
 405 410 415

 Glu Lys Val Leu Gln Gly Asn Ile Thr His Cys Ala Glu Pro Tyr Ile
 420 425 430

 Lys Asn Ser Asp Pro Val Lys Thr Ala Gln Lys Val His Arg Thr Ala
 435 440 445

 Lys Gln Val Cys Ser Arg Leu Gly Gln Tyr Arg Met Pro Phe Ala Trp
 450 455 460

 Ala Ala Arg Pro Ile Phe Lys Asp Thr Gln Gly Ser Leu Asp Leu Asp
 465 470 475 480

 Gly Arg Phe Ser Pro Leu Tyr Lys Gln Asp Ser Ser Lys Leu Ser Ser
 485 490 495

 Glu Asp Ile Leu Lys Leu Leu Ser Glu Tyr Lys Lys Pro Glu Lys Thr
 500 505 510

 Lys Leu Gln Ile Ile Pro Gly Gln Leu Asn Ile Thr Val Glu Cys Val
 515 520 525

 Pro Val Asp Leu Ser Asn Cys Ile Thr Ser Ser Tyr Val Pro Leu Lys
 530 535 540

 Pro Phe Glu Lys Asn Cys Gln Asn Ile Thr Val Glu Val Glu Glu Phe
 545 550 555 560

 Val Pro Glu Met Thr Lys Tyr Cys Tyr Pro Phe Thr Ile Tyr Lys Asn
 565 570 575

 His Leu Tyr Val Tyr Pro Leu Gln Leu Lys Tyr Asp Ser Gln Lys Thr
 580 585 590

 Phe Ala Lys Ala Arg Asn Ile Ala Val Cys Val Glu Phe Arg Asp Ser
 595 600 605

 Asp Glu Ser Asp Ala Ser Ala Leu Lys Cys Ile Tyr Gly Lys Pro Ala
 610 615 620

 Gly Ser Val Phe Thr Thr Asn Ala Tyr Ala Val Val Ser His His Asn
 625 630 635 640

 Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile Glu Leu Pro Ile His
 645 650 655

 Leu His Gln Lys His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys
 660 665 670

 Glu Ile Asn Thr Lys Gly Thr Thr Lys Lys Gln Asp Thr Val Glu Thr
 675 680 685

 Pro Val Gly Phe Ala Trp Val Pro Leu Leu Lys Asp Gly Arg Ile Ile
 690 695 700

 Thr Phe Glu Gln Gln Leu Pro Val Ser Ala Asn Leu Pro Pro Gly Tyr
 705 710 715 720

Leu Asn Leu Asn Asp Ala Glu Ser Arg Arg Gln Cys Asn Val Asp Ile
 725 730 735
 Lys Trp Val Asp Gly Ala Lys Pro Leu Leu Lys Phe Lys Ser His Leu
 740 745 750
 Glu Ser Thr Ile Tyr Thr Gln Asp Leu His Val His Lys Phe Phe His
 755 760 765
 His Cys Gln Leu Ile Gln Ser Gly Ser Lys Glu Val Pro Gly Glu Leu
 770 775 780
 Ile Lys Tyr Leu Lys Cys Leu His Ala Met Glu Ile Gln Val Met Ile
 785 790 795 800
 Gln Phe Leu Pro Val Ile Leu Met Gln Leu Phe Arg Val Leu Thr Asn
 805 810 815
 Met Thr His Glu Asp Asp Val Pro Ile Asn Cys Thr Met Val Leu Leu
 820 825 830
 His Ile Val Ser Lys Cys His Glu Glu Gly Leu Asp Ser Tyr Leu Arg
 835 840 845
 Ser Phe Ile Lys Tyr Ser Phe Arg Pro Glu Lys Pro Ser Ala Pro Gln
 850 855 860
 Ala Gln Leu Ile His Glu Thr Leu Ala Thr Thr Met Ile Ala Ile Leu
 865 870 875 880
 Lys Gln Ser Ala Asp Phe Leu Ser Ile Asn Lys Leu Leu Lys Tyr Ser
 885 890 895
 Trp Phe Phe Phe Glu Ile Ile Ala Lys Ser Met Ala Thr Tyr Leu Leu
 900 905 910
 Glu Glu Asn Lys Ile Lys Leu Pro Arg Gly Gln Arg Phe Pro Glu Thr
 915 920 925
 Tyr His His Val Leu His Ser Leu Leu Leu Ala Ile Ile Pro His Val
 930 935 940
 Thr Ile Arg Tyr Ala Glu Ile Pro Asp Glu Ser Arg Asn Val Asn Tyr
 945 950 955 960
 Ser Leu Ala Ser Phe Leu Lys Arg Cys Leu Thr Leu Met Asp Arg Gly
 965 970 975
 Phe Ile Phe Asn Leu Ile Asn Asp Tyr Ile Ser Gly Phe Ser Pro Lys
 980 985 990
 Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe Glu Phe Leu Gln Thr Ile
 995 1000 1005
 Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met Ala Phe Ala
 1010 1015 1020
 Lys Pro Lys Leu Gln Arg Val Gln Asp Ser Asn Leu Glu Tyr Ser Leu
 1025 1030 1035 1040

Ser Asp Glu Tyr Cys Lys His His Phe Leu Val Gly Leu Leu Leu Arg
 1045 1050 1055
 Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr Glu Ile Arg Tyr Thr Ala
 1060 1065 1070
 Ile Ser Val Ile Lys Asn Leu Leu Ile Lys His Ala Phe Asp Thr Arg
 1075 1080 1085
 Tyr Gln His Lys Asn Gln Gln Ala Lys Ile Ala Gln Leu Tyr Leu Pro
 1090 1095 1100
 Phe Val Gly Leu Leu Leu Glu Asn Ile Gln Arg Leu Ala Gly Arg Asp
 1105 1110 1115 1120
 Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn Ser Ala Ser Arg Asp Glu
 1125 1130 1135
 Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn Arg Gly Ser Leu Ser Thr
 1140 1145 1150
 Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln Asn Gly His Gly Ile Lys
 1155 1160 1165
 Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro Glu Gly Ala Thr Gly Phe
 1170 1175 1180
 Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr Arg Gln Ser Ser Thr Arg
 1185 1190 1195 1200
 Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp Gln Tyr Glu Ile Arg Ser
 1205 1210 1215
 Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys Met Ile Ser Glu Asp Thr
 1220 1225 1230
 Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro Gln Glu Leu Ile Asn Ile
 1235 1240 1245
 Leu Ile Leu Leu Glu Val Cys Leu Phe His Phe Arg Tyr Met Gly Lys
 1250 1255 1260
 Arg Asn Ile Ala Arg Val His Asp Ala Trp Leu Ser Lys His Phe Gly
 1265 1270 1275 1280
 Ile Asp Arg Lys Ser Gln Thr Met Pro Ala Leu Arg Asn Arg Ser Gly
 1285 1290 1295
 Val Met Gln Ala Arg Leu Gln His Leu Ser Ser Leu Glu Ser Ser Phe
 1300 1305 1310
 Thr Leu Asn His Ser Ser Thr Thr Glu Ala Asp Ile Phe His Gln
 1315 1320 1325
 Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu Val Ser Leu Thr Val Leu
 1330 1335 1340
 Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe Lys Thr Gln Leu Leu Asn
 1345 1350 1355 1360

Asn Asp Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Ile His Leu
 1365 1370 1375

 Ala Phe Leu Lys Asn Gly Gln Ser Glu Val Ser Leu Lys His Val Phe
 1380 1385 1390

 Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe Pro Ser Ala Phe Phe Lys
 1395 1400 1405

 Gly Arg Val Asn Met Cys Ala Ala Phe Cys Tyr Glu Val Leu Lys Cys
 1410 1415 1420

 Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn Glu Ala Ser Ala Leu Leu
 1425 1430 1435 1440

 Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr Thr Lys Arg Lys Thr Phe
 1445 1450 1455

 Leu Arg Thr His Leu Gln Ile Ile Ala Val Ser Gln Leu Ile Ala
 1460 1465 1470

 Asp Val Ala Leu Ser Gly Gly Ser Arg Phe Gln Glu Ser Leu Phe Ile
 1475 1480 1485

 Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro Met Lys Ala Thr Ala Phe
 1490 1495 1500

 Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met
 1505 1510 1515 1520

 Ala Thr Ala Gln Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Ile
 1525 1530 1535

 Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu
 1540 1545 1550

 Arg Lys Thr Trp Leu Asp Ser Met Ala Lys Ile His Val Lys Asn Gly
 1555 1560 1565

 Asp Phe Ser Glu Ala Ala Met Cys Tyr Val His Val Ala Ala Leu Val
 1570 1575 1580

 Ala Glu Phe Leu His Arg Lys Lys Leu Phe Pro Asn Gly Cys Ser Ala
 1585 1590 1595 1600

 Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu Glu Gly Ala Met Lys Glu
 1605 1610 1615

 Asp Ala Gly Met Met Asp Val His Tyr Ser Glu Glu Val Leu Leu Glu
 1620 1625 1630

 Leu Leu Glu Gln Cys Val Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu
 1635 1640 1645

 Ile Ile Ser Glu Ile Ser Lys Leu Ile Val Pro Ile Tyr Glu Lys Arg
 1650 1655 1660

 Arg Glu Phe Glu Lys Leu Thr Gln Val Tyr Arg Thr Leu His Gly Ala
 1665 1670 1675 1680

Tyr Thr Lys Ile Leu Glu Val Met His Thr Lys Lys Arg Leu Leu Gly
 1685 1690 1695
 Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu
 1700 1705 1710
 Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser
 1715 1720 1725
 Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr Gly Glu Lys Phe Gly Thr
 1730 1735 1740
 Glu Asn Val Lys Ile Ile Gln Asp Ser Asp Lys Val Asn Ala Lys Glu
 1745 1750 1755 1760
 Leu Asp Pro Lys Tyr Ala His Ile Gln Val Thr Tyr Val Lys Pro Tyr
 1765 1770 1775
 Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys Thr Glu Phe Glu Arg Asn
 1780 1785 1790
 His Asn Ile Ser Arg Phe Val Phe Glu Ala Pro Tyr Thr Leu Ser Gly
 1795 1800 1805
 Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu
 1810 1815 1820
 Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg Ile Pro Ile Asn
 1825 1830 1835 1840
 Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Gly Ala Thr Asp Glu
 1845 1850 1855
 Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys Leu Cys Ser Ser Thr Asp
 1860 1865 1870
 Val Asp Met Ile Gln Leu Gln Leu Lys Leu Gln Gly Trp Val Ser Val
 1875 1880 1885
 Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp
 1890 1895 1900
 Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp
 1905 1910 1915 1920
 Met Phe Arg Lys Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu Leu Asn
 1925 1930 1935
 Glu Arg Leu Ile Lys Glu Asp Gln Val Glu Tyr His Glu Gly Leu Lys
 1940 1945 1950
 Ser Asn Phe Arg Asp Met Val Lys Glu Leu Ser Asp Ile Ile His Glu
 1955 1960 1965
 Gln Ile Leu Gln Glu Asp Thr Met His Ser Pro Trp Met Ser Asn Thr
 1970 1975 1980
 Leu His Val Phe Cys Ala Ile Ser Gly Thr Ser Ser Asp Arg Gly Tyr
 1985 1990 1995 2000

Gly Ser Pro Arg Tyr Ala Glu Val
2005

<210> 100
<211> 2015
<212> PRT
<213> Homo sapiens

<220>
<223> human CLASP-5

<400> 100
Met Thr His Leu Asn Ser Leu Asp Val Gln Leu Ala Gln Glu Leu Gly
1 5 10 15

Asp Phe Thr Asp Asp Asp Leu Asp Val Val Phe Thr Pro Lys Glu Cys
20 25 30

Arg Thr Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro
35 40 45

His Val Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val
50 55 60

Asn Arg Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr
65 70 75 80

Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu
85 90 95

Ser Glu Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg
100 105 110

His Leu Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala
115 120 125

Cys Asp Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn
130 135 140

Leu Leu Gln Gln Val Ser Ala Glu Asp Phe Glu Lys Gln Asn Glu Glu
145 150 155 160

Ala Arg Arg Thr Asn Arg Gln Ala Glu Leu Phe Ala Leu Tyr Pro Ser
165 170 175

Val Asp Glu Glu Asp Ala Val Glu Ile Arg Pro Val Pro Glu Cys Pro
180 185 190

Lys Glu His Leu Gly Asn Arg Ile Leu Val Lys Leu Leu Thr Leu Lys
195 200 205

Phe Glu Ile Glu Ile Glu Pro Leu Phe Ala Ser Ile Ala Leu Tyr Asp
210 215 220

Val Lys Glu Arg Lys Lys Ile Ser Glu Asn Phe His Cys Asp Leu Asn
225 230 235 240

Ser Asp Gln Phe Lys Gly Phe Leu Arg Ala His Thr Pro Ser Val Ala
245 250 255

Ala Ser Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser
 260 265 270
 Ser Asp Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly
 275 280 285
 Asp Ile Gly Asp Cys Ala Glu Pro Tyr Thr Val Ile Lys Glu Ser Asp
 290 295 300
 Gly Gly Lys Ser Lys Glu Lys Ile Glu Lys Leu Lys Leu Gln Ala Glu
 305 310 315 320
 Ser Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp Ala
 325 330 335
 Pro Ile Ser Leu Ser Ser Phe Phe Asn Val Ser Thr Leu Glu Arg Glu
 340 345 350
 Val Thr Asp Val Asp Ser Val Val Gly Arg Ser Pro Val Gly Glu Arg
 355 360 365
 Arg Thr Leu Ala Gln Ser Arg Arg Leu Ser Glu Arg Ala Leu Ser Leu
 370 375 380
 Glu Glu Asn Gly Val Gly Ser Asn Phe Lys Thr Ser Thr Leu Ser Val
 385 390 395 400
 Ser Ser Phe Phe Lys Gln Glu Gly Asp Arg Leu Ser Asp Glu Asp Leu
 405 410 415
 Phe Lys Phe Leu Ala Asp Tyr Lys Arg Ser Ser Ser Leu Gln Arg Arg
 420 425 430
 Val Lys Ser Ile Pro Gly Leu Leu Arg Leu Glu Ile Ser Thr Ala Pro
 435 440 445
 Glu Ile Ile Asn Cys Cys Leu Thr Pro Glu Met Leu Pro Val Lys Pro
 450 455 460
 Phe Pro Glu Asn Arg Thr Arg Pro His Lys Glu Ile Leu Glu Phe Pro
 465 470 475 480
 Thr Arg Glu Val Tyr Val Pro His Thr Val Tyr Arg Asn Leu Leu Tyr
 485 490 495
 Val Tyr Pro Gln Arg Leu Asn Phe Val Asn Lys Leu Ala Ser Ala Arg
 500 505 510
 Asn Ile Thr Ile Lys Ile Gln Phe Met Cys Gly Glu Asp Ala Ser Asn
 515 520 525
 Ala Met Pro Val Ile Phe Gly Lys Ser Ser Gly Pro Glu Phe Leu Gln
 530 535 540
 Glu Val Tyr Thr Ala Val Thr Tyr His Asn Lys Ser Pro Asp Phe Tyr
 545 550 555 560
 Glu Glu Val Lys Ile Lys Leu Pro Ala Lys Leu Thr Val Asn His His
 565 570 575

Leu Leu Phe Thr Phe Tyr His Ile Ser Cys Gln Gln Lys Gln Gly Ala
 580 585 590

 Ser Val Glu Thr Leu Leu Gly Tyr Ser Trp Leu Pro Ile Leu Leu Asn
 595 600 605

 Glu Arg Leu Gln Thr Gly Ser Tyr Cys Leu Pro Val Ala Leu Glu Lys
 610 615 620

 Leu Pro Pro Asn Tyr Ser Met His Ser Ala Glu Lys Val Pro Leu Gln
 625 630 635 640

 Asn Pro Pro Ile Lys Trp Ala Glu Gly His Lys Gly Val Phe Asn Ile
 645 650 655

 Glu Val Gln Ala Val Ser Ser Val His Thr Gln Asp Asn His Leu Glu
 660 665 670

 Lys Phe Phe Thr Leu Cys His Ser Leu Glu Ser Gln Val Thr Phe Pro
 675 680 685

 Ile Arg Val Leu Asp Gln Lys Ile Ser Glu Met Ala Leu Glu His Glu
 690 695 700

 Leu Lys Leu Ser Ile Ile Cys Leu Asn Ser Ser Arg Leu Glu Pro Leu
 705 710 715 720

 Val Leu Phe Leu His Leu Val Leu Asp Lys Leu Phe Gln Leu Ser Val
 725 730 735

 Gln Pro Met Val Ile Ala Gly Gln Thr Ala Asn Phe Ser Gln Phe Ala
 740 745 750

 Phe Glu Ser Val Val Ala Ile Ala Asn Ser Leu His Asn Ser Lys Asp
 755 760 765

 Leu Ser Lys Asp Gln His Gly Arg Asn Cys Leu Leu Ala Ser Tyr Val
 770 775 780

 His Tyr Val Phe Arg Leu Pro Glu Val Gln Arg Asp Val Pro Lys Ser
 785 790 795 800

 Gly Ala Pro Thr Ala Leu Leu Asp Pro Arg Ser Tyr His Thr Tyr Gly
 805 810 815

 Arg Thr Ser Ala Ala Ala Val Ser Ser Lys Leu Leu Gln Ala Arg Val
 820 825 830

 Met Ser Ser Asn Pro Asp Leu Ala Gly Thr His Ser Ala Ala Asp
 835 840 845

 Glu Glu Val Lys Asn Ile Met Ser Ser Lys Ile Ala Asp Arg Asn Cys
 850 855 860

 Ser Arg Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser
 865 870 875 880

 Pro Ala Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu
 885 890 895

Ala Leu Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln
 900 905 910
 His Val His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe
 915 920 925
 Ser Asp Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr
 930 935 940
 Ser Glu Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln
 945 950 955 960
 Ala Glu Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu
 965 970 975
 Ser Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys
 980 985 990
 Ser Gln Leu Ser Ala Lys Leu Ser Asn Leu Pro Thr Leu Ile Ser Met
 995 1000 1005
 Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His Glu His Tyr Leu Asn
 1010 1015 1020
 Leu Asn Leu Phe Phe Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys
 1025 1030 1035 1040
 Pro Ser Ile Ser Ser Gln Asn Ser Ser Cys Ser Ser Phe Gln Asp
 1045 1050 1055
 Gln Lys Ile Ala Ser Met Phe Asp Leu Thr Ser Glu Tyr Arg Gln Gln
 1060 1065 1070
 His Phe Leu Thr Gly Leu Leu Phe Thr Glu Leu Ala Ala Leu Asp
 1075 1080 1085
 Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala
 1090 1095 1100
 Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys
 1105 1110 1115 1120
 Pro Glu Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly
 1125 1130 1135
 Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp
 1140 1145 1150
 Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala
 1155 1160 1165
 Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe
 1170 1175 1180
 Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln
 1185 1190 1195 1200
 Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe
 1205 1210 1215

Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile
1220 1225 1230

Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe
1235 1240 1245

Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys
1250 1255 1260

Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu
1265 1270 1275 1280

Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg
1285 1290 1295

Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu
1300 1305 1310

Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu
1315 1320 1325

Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn
1330 1335 1340

Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile
1345 1350 1355 1360

Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly
1365 1370 1375

Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr
1380 1385 1390

Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe
1395 1400 1405

Gly Asp Leu Leu Phe Glu Glu Val Glu Gln Cys Phe Asp Leu Cys
1410 1415 1420

His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser
1425 1430 1435 1440

Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala
1445 1450 1455

Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala
1460 1465 1470

Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg
1475 1480 1485

Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln
1490 1495 1500

Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn
1505 1510 1515 1520

Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro
1525 1530 1535

Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala
 1540 1545 1550
 Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His
 1555 1560 1565
 Thr Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala
 1570 1575 1580
 Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr
 1585 1590 1595 1600
 Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu
 1605 1610 1615
 Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly
 1620 1625 1630
 Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu
 1635 1640 1645
 Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val
 1650 1655 1660
 Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu
 1665 1670 1675 1680
 Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp
 1685 1690 1695
 Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg
 1700 1705 1710
 Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe
 1715 1720 1725
 Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
 1730 1735 1740
 Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
 1745 1750 1755 1760
 Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys
 1765 1770 1775
 Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu
 1780 1785 1790
 Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg
 1795 1800 1805
 Phe Met Tyr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu
 1810 1815 1820
 Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala
 1825 1830 1835 1840
 Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe
 1845 1850 1855

Val	Leu	Thr	Pro	Ile	Glu	Val	Ala	Ile	Glu	Asp	Met	Lys	Lys	Lys	Thr
1860						1865						1870			
Leu	Gln	Leu	Ala	Val	Ala	Ile	Asn	Gln	Glu	Pro	Pro	Asp	Ala	Lys	Met
1875							1880						1885		
Leu	Gln	Met	Val	Leu	Gln	Gly	Ser	Val	Gly	Ala	Thr	Val	Asn	Gln	Gly
1890						1895						1900			
Pro	Leu	Glu	Val	Ala	Gln	Val	Phe	Leu	Ala	Glu	Ile	Pro	Ala	Asp	Pro
1905						1910					1915			1920	
Lys	Leu	Tyr	Arg	His	His	Asn	Lys	Leu	Arg	Leu	Cys	Phe	Lys	Glu	Phe
1925						1930						1935			
Ile	Met	Arg	Cys	Gly	Glu	Ala	Val	Glu	Lys	Asn	Lys	Arg	Leu	Ile	Thr
1940						1945						1950			
Ala	Asp	Gln	Arg	Glu	Tyr	Gln	Glu	Leu	Lys	Lys	Asn	Tyr	Asn	Lys	
1955						1960					1965				
Leu	Lys	Glu	Asn	Leu	Arg	Pro	Met	Ile	Glu	Arg	Lys	Ile	Pro	Glu	Leu
1970						1975					1980				
Tyr	Lys	Pro	Ile	Phe	Arg	Val	Glu	Ser	Gln	Lys	Arg	Asp	Ser	Phe	His
1985						1990					1995			2000	
Arg	Ser	Ser	Phe	Arg	Lys	Cys	Glu	Thr	Gln	Leu	Ser	Gln	Gly	Ser	
2005						2010						2015			

<210> 101

<211> 2090

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-3

<400> 101

Met	Ala	Glu	Arg	Arg	Ala	Phe	Ala	Gln	Lys	Ile	Ser	Arg	Thr	Val	Ala
1						5				10				15	

Ala	Glu	Val	Arg	Lys	Gln	Ile	Ser	Gly	Gln	Tyr	Ser	Gly	Ser	Pro	Gln
						20			25				30		

Leu	Leu	Lys	Asn	Leu	Asn	Ile	Val	Gly	Asn	Ile	Ser	His	His	Thr	Thr
						35			40			45			

Val	Pro	Leu	Thr	Glu	Ala	Val	Asp	Pro	Val	Asp	Leu	Glu	Asp	Tyr	Leu
						50			55			60			

Ile	Thr	His	Pro	Leu	Ala	Val	Asp	Ser	Gly	Pro	Leu	Arg	Asp	Leu	Ile
						65			70			75			80

Glu	Phe	Pro	Pro	Asp	Asp	Ile	Glu	Val	Val	Tyr	Ser	Pro	Arg	Asp	Cys
						85			90			95			

Arg	Thr	Leu	Val	Ser	Ala	Val	Pro	Glu	Glu	Ser	Glu	Met	Asp	Pro	His
						100			105			110			

Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu Asp Trp Ala Ile Val Ile
 115 120 125
 Arg Lys Tyr His Lys Leu Gly Thr Gly Phe Asn Pro Asn Thr Leu Asp
 130 135 140
 Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro Lys Gln Val Phe Glu Ser
 145 150 155 160
 Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln Asp Asp Gln Asp Asp Leu
 165 170 175
 Lys Arg Arg Ser Met Ser Ile Asp Asp Thr Pro Arg Gly Ser Trp Ala
 180 185 190
 Cys Ser Ile Phe Asp Leu Lys Asn Ser Leu Pro Asp Ala Leu Leu Pro
 195 200 205
 Asn Leu Leu Asp Arg Thr Pro Asn Glu Glu Ile Asp Arg Gln Asn Asp
 210 215 220
 Asp Gln Arg Lys Ser Asn Arg His Lys Glu Leu Phe Ala Leu His Pro
 225 230 235 240
 Ser Pro Asp Glu Glu Glu Pro Ile Glu Arg Leu Ser Val Pro Asp Ile
 245 250 255
 Pro Lys Glu His Phe Gly Gln Arg Leu Leu Val Lys Cys Leu Ser Leu
 260 265 270
 Lys Phe Glu Ile Glu Ile Glu Pro Ile Phe Ala Ser Leu Ala Leu Tyr
 275 280 285
 Asp Val Lys Glu Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu
 290 295 300
 Asn Ser Glu Gln Met Lys Gly Leu Leu Arg Pro His Val Pro Pro Ala
 305 310 315 320
 Ala Ile Thr Thr Leu Ala Arg Ser Ala Ile Phe Ser Ile Thr Tyr Pro
 325 330 335
 Ser Gln Asp Val Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln
 340 345 350
 Gly Asp Ile Gly Glu Cys Ala Glu Pro Tyr Met Ile Phe Lys Glu Ala
 355 360 365
 Asp Ala Thr Lys Asn Lys Glu Lys Leu Glu Lys Leu Lys Ser Gln Ala
 370 375 380
 Asp Gln Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp
 385 390 395 400
 Thr Ala Ile His Leu Met Asn Ile Val Ser Ser Ala Gly Ser Leu Glu
 405 410 415
 Arg Asp Ser Thr Glu Val Glu Ile Ser Thr Gly Glu Arg Lys Gly Ser
 420 425 430

Trp Ser Glu Arg Arg Asn Ser Ser Ile Val Gly Arg Arg Ser Leu Glu
435 440 445

Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn Leu Thr Ser Phe Arg Pro
450 455 460

Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Gly Asp Arg Leu
465 470 475 480

Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala Asp Met Arg Arg Pro Ser
485 490 495

Ser Val Leu Arg Arg Leu Arg Pro Ile Thr Ala Gln Leu Lys Ile Asp
500 505 510

Ile Ser Pro Ala Pro Glu Asn Pro His Tyr Cys Leu Thr Pro Glu Leu
515 520 525

Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg Val Arg Pro Thr Arg Glu
530 535 540

Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr Val Pro Asn Thr Thr Tyr
545 550 555 560

Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser Leu Asn Phe Ala Asn Arg
565 570 575

Gln Gly Ser Ala Arg Asn Ile Thr Val Lys Val Gln Phe Met Tyr Gly
580 585 590

Glu Asp Pro Ser Asn Ala Met Pro Val Ile Phe Gly Lys Ser Ser Cys
595 600 605

Ser Glu Phe Ser Lys Glu Ala Tyr Thr Ala Val Val Tyr His Asn Arg
610 615 620

Ser Pro Asp Phe His Glu Glu Ile Lys Val Lys Leu Pro Ala Thr Leu
625 630 635 640

Thr Asp His His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys Gln
645 650 655

Gln Lys Gln Asn Thr Pro Leu Glu Thr Pro Val Gly Tyr Thr Trp Ile
660 665 670

Pro Met Leu Gln Asn Gly Arg Leu Lys Thr Gly Gln Phe Cys Leu Pro
675 680 685

Val Ser Leu Glu Lys Pro Pro Gln Ala Tyr Ser Val Leu Ser Pro Glu
690 695 700

Val Pro Leu Pro Gly Met Lys Trp Val Asp Asn His Lys Gly Val Phe
705 710 715 720

Asn Val Glu Val Val Ala Val Ser Ser Ile His Thr Gln Asp Pro Tyr
725 730 735

Leu Asp Lys Phe Phe Ala Leu Val Asn Ala Leu Asp Glu His Leu Phe
740 745 750

Pro Val Arg Ile Gly Asp Met Arg Ile Met Glu Asn Asn Leu Glu Asn
 755 760 765
 Glu Leu Lys Ser Ser Ile Ser Ala Leu Asn Ser Ser Gln Leu Glu Pro
 770 775 780
 Val Val Arg Phe Leu His Leu Leu Leu Asp Lys Leu Ile Leu Leu Val
 785 790 795 800
 Ile Arg Pro Pro Val Ile Ala Gly Gln Ile Val Asn Leu Gly Gln Ala
 805 810 815
 Ser Phe Glu Ala Met Ala Ser Ile Ile Asn Arg Leu His Lys Asn Leu
 820 825 830
 Glu Gly Asn His Asp Gln His Gly Arg Asn Ser Leu Leu Ala Ser Tyr
 835 840 845
 Ile His Tyr Val Phe Arg Leu Pro Asn Thr Tyr Pro Asn Ser Ser Ser
 850 855 860
 Pro Gly Pro Gly Gly Leu Gly Gly Ser Val His Tyr Ala Thr Met Ala
 865 870 875 880
 Arg Ser Ala Val Arg Pro Ala Ser Leu Asn Leu Asn Arg Ser Arg Ser
 885 890 895
 Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly Thr Pro Thr Ser Pro Asp
 900 905 910
 Asp Glu Val Arg Ser Ile Ile Gly Ser Lys Gly Leu Asp Arg Ser Asn
 915 920 925
 Ser Trp Val Asn Thr Gly Gly Pro Lys Ala Ala Pro Trp Gly Ser Asn
 930 935 940
 Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala Met Asp Arg Ser Cys Asn
 945 950 955 960
 Arg Met Ser Ser His Thr Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr
 965 970 975
 Gly Arg Leu Pro Thr Lys Lys Leu Phe His Glu Glu Leu Ala Leu Gln
 980 985 990
 Trp Val Val Cys Ser Gly Ser Val Arg Glu Ser Ala Leu Gln Gln Ala
 995 1000 1005
 Trp Phe Phe Phe Glu Leu Met Val Lys Ser Met Val His His Leu Tyr
 1010 1015 1020
 Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg
 1025 1030 1035 1040
 Phe Met Asp Asp Ile Ala Ala Leu Val Ser Thr Ile Ala Ser Asp Ile
 1045 1050 1055
 Val Ser Arg Phe Gln Lys Asp Thr Glu Met Val Glu Arg Leu Asn Thr
 1060 1065 1070

Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu Ser Val Met Asp Arg Gly
1075 1080 1085

Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys
1090 1095 1100

Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu Val Ser Leu Arg Leu Asp
1105 1110 1115 1120

Phe Leu Arg Ile Ile Cys Ser His Glu His Tyr Val Thr Leu Asn Leu
1125 1130 1135

Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser Pro Ser Pro Val Ser
1140 1145 1150

Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser Thr Asn Val Gln Asp Gln
1155 1160 1165

Lys Ile Ala Asn Met Phe Glu Leu Ser Val Pro Phe Arg Gln Gln His
1170 1175 1180

Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu Ala Val Ile Leu Asp Pro
1185 1190 1195 1200

Asp Ala Glu Gly Leu Phe Gly Leu His Lys Lys Val Ile Asn Met Val
1205 1210 1215

His Asn Leu Leu Ser Ser His Asp Ser Asp Pro Arg Tyr Ser Asp Pro
1220 1225 1230

Gln Ile Lys Ala Arg Val Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile
1235 1240 1245

Ile Met Glu Thr Val Pro Gln Leu Tyr Asp Phe Thr Glu Thr His Asn
1250 1255 1260

Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu
1265 1270 1275 1280

Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr
1285 1290 1295

Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr
1300 1305 1310

Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu
1315 1320 1325

Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu
1330 1335 1340

Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu
1345 1350 1355 1360

Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys
1365 1370 1375

Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met
1380 1385 1390

Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln
 1395 1400 1405
 Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly
 1410 1415 1420
 Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr
 1425 1430 1435 1440
 His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile
 1445 1450 1455
 Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu
 1460 1465 1470
 Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr
 1475 1480 1485
 Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His
 1490 1495 1500
 Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala
 1505 1510 1515 1520
 Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu
 1525 1530 1535
 Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys
 1540 1545 1550
 Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr
 1555 1560 1565
 Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val
 1570 1575 1580
 Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln
 1585 1590 1595 1600
 Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr
 1605 1610 1615
 Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln
 1620 1625 1630
 Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val
 1635 1640 1645
 Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met
 1650 1655 1660
 Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp
 1665 1670 1675 1680
 Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu
 1685 1690 1695
 Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu
 1700 1705 1710

Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe
 1715 1720 1725
 Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp
 1730 1735 1740
 Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr
 1745 1750 1755 1760
 Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser
 1765 1770 1775
 Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile
 1780 1785 1790
 Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His
 1795 1800 1805
 Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly
 1810 1815 1820
 Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr
 1825 1830 1835 1840
 Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala
 1845 1850 1855
 Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly
 1860 1865 1870
 Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro
 1875 1880 1885
 Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr
 1890 1895 1900
 Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr
 1905 1910 1915 1920
 Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro
 1925 1930 1935
 Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys
 1940 1945 1950
 Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr
 1955 1960 1965
 Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu
 1970 1975 1980
 Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala
 1985 1990 1995 2000
 Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln
 2005 2010 2015
 Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln
 2020 2025 2030

Val	Phe	Leu	Ser	Glu	Ile	Pro	Ser	Asp	Pro	Lys	Leu	Phe	Arg	His	His
2035						2040						2045			
Asn	Lys	Leu	Arg	Leu	Cys	Phe	Lys	Asp	Phe	Thr	Lys	Arg	Cys	Glu	Asp
2050						2055						2060			
Ala	Leu	Arg	Lys	Asn	Lys	Ser	Leu	Ile	Gly	Pro	Val	Gln	Lys	Glu	Tyr
2065						2070						2075			2080
Gln	Arg	Glu	Leu	Gly	Lys	Leu	Ser	Ser	Pro						
						2085						2090			
<210> 102															
<211> 1980															
<212> PRT															
<213> Homo sapiens															
<220>															
<223> human CLASP-2															
<400> 102															
Met	Leu	Leu	Phe	Pro	Tyr	Asp	Asp	Phe	Gln	Thr	Ala	Ile	Leu	Arg	Arg
1									10					15	
Gln	Gly	Arg	Tyr	Ile	Cys	Ser	Thr	Val	Pro	Ala	Lys	Ala	Glu	Glu	Glu
									25				30		
Ala	Gln	Ser	Leu	Phe	Val	Thr	Glu	Cys	Ile	Lys	Thr	Tyr	Asn	Ser	Asp
									40				45		
Trp	His	Leu	Val	Asn	Tyr	Lys	Tyr	Glu	Asp	Tyr	Ser	Gly	Glu	Phe	Arg
									55				60		
Gln	Leu	Pro	Asn	Lys	Val	Val	Lys	Leu	Asp	Lys	Leu	Pro	Val	His	Val
									70				75		80
Tyr	Glu	Val	Asp	Glu	Glu	Val	Asp	Lys	Asp	Glu	Asp	Ala	Ala	Ser	Leu
									85				90		95
Gly	Ser	Gln	Lys	Gly	Gly	Ile	Thr	Lys	His	Gly	Trp	Leu	Tyr	Lys	Gly
									100				105		110
Asn	Met	Asn	Ser	Ala	Ile	Ser	Val	Thr	Met	Arg	Ser	Phe	Lys	Arg	Arg
									115				120		125
Phe	Phe	His	Leu	Ile	Gln	Leu	Gly	Asp	Gly	Ser	Tyr	Asn	Leu	Asn	Phe
									130				135		140
Tyr	Lys	Asp	Glu	Lys	Ile	Ser	Lys	Glu	Pro	Lys	Gly	Ser	Ile	Phe	Leu
									145				150		160
Asp	Ser	Cys	Met	Gly	Val	Val	Gln	Asn	Asn	Lys	Val	Arg	Arg	Phe	Ala
									165				170		175
Phe	Glu	Leu	Lys	Met	Gln	Asp	Lys	Ser	Ser	Tyr	Leu	Leu	Ala	Ala	Asp
									180				185		190
Ser	Glu	Val	Glu	Met	Glu	Glu	Trp	Ile	Thr	Ile	Leu	Asn	Lys	Ile	Leu
									195				200		205

Gln Leu Asn Phe Glu Ala Ala Met Gln Glu Lys Arg Asn Gly Asp Ser
 210 215 220
 His Glu Asp Asp Glu Gln Ser Lys Leu Glu Gly Ser Gly Ser Gly Leu
 225 230 235 240
 Asp Ser Tyr Leu Pro Glu Leu Ala Lys Ser Ala Arg Glu Ala Glu Ile
 245 250 255
 Lys Leu Lys Ser Glu Ser Arg Val Lys Leu Phe Tyr Leu Asp Pro Asp
 260 265 270
 Ala Gln Lys Leu Asp Phe Ser Ser Ala Glu Pro Glu Val Lys Ser Phe
 275 280 285
 Glu Glu Lys Phe Gly Lys Arg Ile Leu Val Lys Cys Asn Asp Leu Ser
 290 295 300
 Phe Asn Leu Gln Cys Cys Val Ala Glu Asn Glu Glu Gly Pro Thr Thr
 305 310 315 320
 Asn Val Glu Pro Phe Phe Val Thr Leu Ser Leu Phe Asp Ile Lys Tyr
 325 330 335
 Asn Arg Lys Ile Ser Ala Asp Phe His Val Asp Leu Asn His Phe Ser
 340 345 350
 Val Arg Gln Met Leu Ala Thr Thr Ser Pro Ala Leu Met Asn Gly Ser
 355 360 365
 Gly Gln Ser Pro Ser Val Leu Lys Gly Ile Leu His Glu Ala Ala Met
 370 375 380
 Gln Tyr Pro Lys Gln Gly Ile Phe Ser Val Thr Cys Pro His Pro Asp
 385 390 395 400
 Ile Phe Leu Val Ala Arg Ile Glu Lys Val Leu Gln Gly Ser Ile Thr
 405 410 415
 His Cys Ala Glu Pro Tyr Met Lys Ser Ser Asp Ser Ser Lys Val Ala
 420 425 430
 Gln Lys Val Leu Lys Asn Ala Lys Gln Ala Cys Gln Arg Leu Gly Gln
 435 440 445
 Tyr Arg Met Pro Phe Ala Trp Ala Ala Arg Thr Leu Phe Lys Asp Ala
 450 455 460
 Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg Gln
 465 470 475 480
 Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala Asp
 485 490 495
 Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly Asn
 500 505 510
 Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr Val
 515 520 525

Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys Thr
 530 535 540
 Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys His
 545 550 555 560
 Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro Lys
 565 570 575
 Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn Ile
 580 585 590
 Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln Pro
 595 600 605
 Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg Ser
 610 615 620
 Ala Phe Ala Ala Val Leu His His Gln Asn Pro Glu Phe Tyr Asp
 625 630 635 640
 Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu
 645 650 655
 Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser
 660 665 670
 Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu
 675 680 685
 Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro
 690 695 700
 Val Ser Ala Asn Leu Pro Ser Gly His Leu Gly Tyr Gln Glu Leu Gly
 705 710 715 720
 Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys
 725 730 735
 Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln
 740 745 750
 Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser
 755 760 765
 Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu
 770 775 780
 His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu
 785 790 795 800
 Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala
 805 810 815
 Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu
 820 825 830 835
 Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys
 835 840 845

Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu
 850 855 860
 Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr
 865 870 875 880
 Ser Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile
 885 890 895
 Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu
 900 905 910
 Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val
 915 920 925
 Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro
 930 935 940
 Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg
 945 950 955 960
 Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn
 965 970 975
 Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr
 980 985 990
 Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro
 995 1000 1005
 Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln
 1010 1015 1020
 Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His
 1025 1030 1035 1040
 Phe Leu Val Gly Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu
 1045 1050 1055
 Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu
 1060 1065 1070
 Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala
 1075 1080 1085
 Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn
 1090 1095 1100
 Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala
 1105 1110 1115 1120
 Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro
 1125 1130 1135
 Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys
 1140 1145 1150
 Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser
 1155 1160 1165

Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu
 1170 1175 1180
 Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys
 1185 1190 1195 1200
 Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser
 1205 1210 1215
 Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu
 1220 1225 1230
 Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe
 1235 1240 1245
 Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr
 1250 1255 1260
 Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr
 1265 1270 1275 1280
 Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys
 1285 1290 1295
 Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala
 1300 1305 1310
 Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His
 1315 1320 1325
 Ser Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu
 1330 1335 1340
 Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser
 1345 1350 1355 1360
 Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His
 1365 1370 1375
 Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln
 1380 1385 1390
 Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg
 1395 1400 1405
 Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp
 1410 1415 1420
 Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys
 1425 1430 1435 1440
 Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met
 1445 1450 1455
 Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His
 1460 1465 1470
 Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly
 1475 1480 1485

Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys
 1490 1495 1500

 Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val
 1505 1510 1515 1520

 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1525 1530 1535

 Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1540 1545 1550

 Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp
 1555 1560 1565

 Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu
 1570 1575 1580

 Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu
 1585 1590 1595 1600

 Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 1605 1610 1615

 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 1620 1625 1630

 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
 1635 1640 1645

 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp
 1650 1655 1660

 Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe
 1665 1670 1675 1680

 Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr
 1685 1690 1695

 Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys
 1700 1705 1710

 Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn
 1715 1720 1725

 Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val
 1730 1735 1740

 Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe
 1745 1750 1755 1760

 Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr
 1765 1770 1775

 Gln Thr Gly Lys Arg Gln Gly Val Glu Glu Gln Cys Lys Arg Arg
 1780 1785 1790

 Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile
 1795 1800 1805

Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala
 1810 1815 1820
 Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser
 1825 1830 1835 1840
 Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser
 1845 1850 1855
 Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe
 1860 1865 1870
 Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu
 1875 1880 1885
 Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu
 1890 1895 1900
 Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu
 1905 1910 1915 1920
 Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile
 1925 1930 1935
 Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro
 1940 1945 1950
 Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr
 1955 1960 1965
 Met Val His Gly Met Thr Ser Ser Ser Val Val
 1970 1975 1980

<210> 103

<211> 2045

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-7

<400> 103

Met Ala Ala Ser Glu Arg Arg Ala Phe Ala His Lys Ile Asn Arg Thr
 1 5 10 15

Val Ala Ala Glu Val Arg Lys Gln Val Ser Arg Glu Arg Ser Gly Ser
 20 25 30

Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val Pro Leu Thr
 35 40 45

Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro
 50 55 60

Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala
 65 70 75 80

Asp Asp Leu Glu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu
 85 90 95

Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val Arg Ala Ala
 100 105 110
 Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg Arg Tyr Gln
 115 120 125
 Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr Gln Arg Glu
 130 135 140
 Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp Ala Ser Gly
 145 150 155 160
 Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg Arg Gly Ser
 165 170 175
 Gly Ser Pro Glu Asp Thr Pro Arg Ser Ser Gly Ala Ser Ser Ile Phe
 180 185 190
 Asp Leu Arg Asn Leu Ala Ala Asp Ser Leu Leu Pro Ser Leu Leu Glu
 195 200 205
 Arg Ala Ala Pro Glu Asp Val Asp Arg Arg Asn Glu Thr Leu Arg Arg
 210 215 220
 Gln His Arg Pro Pro Ala Leu Leu Thr Leu Tyr Pro Ala Pro Asp Glu
 225 230 235 240
 Asp Glu Ala Val Glu Arg Cys Ser Arg Pro Glu Pro Pro Arg Glu His
 245 250 255
 Phe Gly Gln Arg Ile Leu Val Lys Cys Leu Ser Leu Lys Phe Glu Ile
 260 265 270
 Glu Ile Glu Pro Ile Phe Gly Ile Leu Ala Leu Tyr Asp Val Arg Glu
 275 280 285
 Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn Ser Asp Ser
 290 295 300
 Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala Ile Ser Thr
 305 310 315 320
 Leu Ala Arg Ser Ala Ile Phe Ser Val Thr Tyr Pro Ser Pro Asp Ile
 325 330 335
 Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly Asp Ile Ser
 340 345 350
 Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp Thr Ala Lys
 355 360 365
 Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu Gln Phe Cys
 370 375 380
 Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr Ala Val His
 385 390 395 400
 Leu Ala Asn Ile Val Ser Ser Ala Gly Gln Leu Asp Arg Asp Ser Asp
 405 410 415

Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Arg Gly
 420 425 430

 Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly
 435 440 445

 Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala
 450 455 460

 Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg
 465 470 475 480

 Arg Pro Ser Ser Leu Leu Arg Arg Leu Arg Pro Val Thr Ala Gln Leu
 485 490 495

 Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser
 500 505 510

 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro
 515 520 525

 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
 530 535 540

 Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe
 545 550 555 560

 Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr
 565 570 575

 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys
 580 585 590

 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr
 595 600 605

 His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro
 610 615 620

 Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val
 625 630 635 640

 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe
 645 650 655

 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe
 660 665 670

 Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr Ser Val Leu
 675 680 685

 Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp Gly His Lys
 690 695 700

 Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val His Pro Gln
 705 710 715 720

 Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val Leu Glu Glu
 725 730 735

Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser Glu Gly Asn
 740 745 750

Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg Leu Ala Ser
 755 760 765

Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp Lys Leu Val
 770 775 780

Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile Val Asn Leu
 785 790 795 800

Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser Leu Val His
 805 810 815

Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys Pro Gln Leu
 820 825 830

Ala Ala Tyr Val His Tyr Ala Phe Arg Leu Pro Gly Thr Glu Pro Ser
 835 840 845

Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala Thr Leu Ala
 850 855 860

Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg Ser Lys Ser
 865 870 875 880

Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly Ser Val Asp
 885 890 895

Asp Glu Val Ser Arg Ile Leu Ala Ser Lys Leu Leu His Glu Glu Leu
 900 905 910

Ala Leu Gln Trp Val Val Ser Ser Ala Val Arg Glu Ala Ile Leu
 915 920 925

Gln His Ala Trp Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu
 930 935 940

His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe
 945 950 955 960

Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly
 965 970 975

Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His
 980 985 990

Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val
 995 1000 1005

Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val
 1010 1015 1020

Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu
 1025 1030 1035 1040

Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr
 1045 1050 1055

Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro
 1060 1065 1070
 Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala
 1075 1080 1085
 Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg
 1090 1095 1100
 Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala
 1105 1110 1115 1120
 Leu Gln Glu Asp Gln Asp Val Arg His Leu Ala Leu Ala Val Leu Lys
 1125 1130 1135
 Asn Leu Met Ala Lys His Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg
 1140 1145 1150
 Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu
 1155 1160 1165
 Leu Asp Asn Met Pro Arg Ile Arg Leu His Asp Phe Ala Glu Gly Pro
 1170 1175 1180
 Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr Glu Gly
 1185 1190 1195 1200
 Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met Ala Ile
 1205 1210 1215
 Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser Gln Gly
 1220 1225 1230
 Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu Ser Ser
 1235 1240 1245
 Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr Glu Pro
 1250 1255 1260
 Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln Leu Gly
 1265 1270 1275 1280
 Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu Tyr Lys
 1285 1290 1295
 Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys Lys Ser
 1300 1305 1310
 Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr Ile Gly
 1315 1320 1325
 Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro Phe Gly
 1330 1335 1340
 Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp Lys Gln
 1345 1350 1355 1360
 Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His Glu Ala
 1365 1370 1375

Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val Leu Asp
 1380 1385 1390

 Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala Arg Glu
 1395 1400 1405

 Ser Val Leu Gly Ala Val Leu Lys Val Val Leu Tyr Ser Leu Gly Ser
 1410 1415 1420

 Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu Ala Thr Gln Arg Ala
 1425 1430 1435 1440

 Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr Glu Leu
 1445 1450 1455

 Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser Arg Ile
 1460 1465 1470

 Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu Met Arg
 1475 1480 1485

 Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met Gln Val
 1490 1495 1500

 Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe Ser Glu
 1505 1510 1515 1520

 Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu
 1525 1530 1535

 Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln Asp Leu
 1540 1545 1550

 Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met Lys Glu
 1555 1560 1565

 His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala
 1570 1575 1580

 Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn
 1585 1590 1595 1600

 Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala Ala Gln
 1605 1610 1615

 Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala Leu Leu
 1620 1625 1630

 Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln Asn Ile
 1635 1640 1645

 Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile Leu Ser
 1650 1655 1660

 Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu Leu Gly
 1665 1670 1675 1680

 Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met Gly Gly
 1685 1690 1695

Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro Ile Leu
 1700 1705 1710
 Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly Lys Leu
 1715 1720 1725
 Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp Glu Arg
 1730 1735 1740
 Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His Phe Gly
 1745 1750 1755 1760
 Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile Thr Lys
 1765 1770 1775
 Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu Arg Phe
 1780 1785 1790
 Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val Asp Lys
 1795 1800 1805
 Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu
 1810 1815 1820
 Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr Phe Asp
 1825 1830 1835 1840
 Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe Thr Pro
 1845 1850 1855
 Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg Lys Thr
 1860 1865 1870
 Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg Ile Arg
 1875 1880 1885
 Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val Ala Ile
 1890 1895 1900
 Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr Glu Gln
 1905 1910 1915 1920
 Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly Ser Val
 1925 1930 1935
 Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu
 1940 1945 1950
 Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn Lys Leu
 1955 1960 1965
 Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala Leu Arg
 1970 1975 1980
 Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His Arg Glu
 1985 1990 1995 2000
 Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro Leu Leu
 2005 2010 2015

Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly Leu Arg
2020 2025 2030

Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu
2035 2040 2045

<210> 104
<211> 2180
<212> PRT
<213> Homo sapiens

<220>
<223> human CLASP-1

<400> 104
Met Ser Phe Arg Gly Lys Val Phe Lys Arg Glu Pro Ser Glu Phe Trp
1 5 10 15

Lys Lys Arg Arg Thr Val Arg Arg Val Ile Gln Glu Glu Phe His Arg
20 25 30

Phe Ser Ser Gln Glu Lys Pro Arg Leu Leu Glu Pro Leu Asp Tyr Glu
35 40 45

Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln
50 55 60

Asp Leu Leu Phe Phe Pro Ser Asp Asp Phe Ser Ala Ala Thr Val Ser
65 70 75 80

Trp Asp Ile Arg Thr Leu Tyr Ser Thr Val Pro Glu Asp Ala Glu His
85 90 95

Lys Ala Glu Asn Leu Leu Val Lys Glu Ala Cys Lys Phe Tyr Ser Ser
100 105 110

Gln Trp His Val Val Asn Tyr Lys Tyr Glu Gln Tyr Ser Gly Asp Ile
115 120 125

Arg Gln Leu Pro Arg Ala Glu Tyr Lys Pro Glu Lys Leu Pro Ser His
130 135 140

Ser Phe Glu Ile Asp His Glu Asp Ala Asp Lys Asp Glu Asp Thr Thr
145 150 155 160

Ser His Ser Ser Ser Lys Gly Gly Gly Ala Gly Gly Thr Gly Val
165 170 175

Phe Lys Ser Gly Trp Leu Tyr Lys Gly Asn Phe Asn Ser Thr Val Asn
180 185 190

Asn Thr Val Thr Val Arg Ser Phe Lys Lys Arg Tyr Phe Gln Leu Thr
195 200 205

Gln Leu Pro Asp Asn Ser Tyr Ile Met Asn Phe Tyr Lys Asp Glu Lys
210 215 220

Ile Ser Lys Glu Pro Lys Gly Cys Ile Phe Leu Asp Ser Cys Thr Gly
225 230 235 240

Val Val Gln Asn Asn Arg Leu Arg Lys Tyr Ala Phe Glu Leu Lys Met
 245 250 255
 Asn Asp Leu Thr Tyr Phe Val Leu Ala Ala Glu Thr Glu Ser Asp Met
 260 265 270
 Asp Glu Trp Ile His Thr Leu Asn Arg Ile Leu Gln Ile Ser Pro Glu
 275 280 285
 Gly Pro Leu Gln Gly Arg Arg Ser Thr Glu Leu Thr Asp Leu Gly Leu
 290 295 300
 Asp Ser Leu Asp Asn Ser Val Thr Cys Glu Cys Thr Pro Glu Glu Thr
 305 310 315 320
 Asp Ser Ser Glu Asn Asn Leu His Ala Asp Phe Ala Lys Tyr Leu Thr
 325 330 335
 Glu Thr Glu Asp Thr Val Lys Thr Thr Arg Asn Met Glu Arg Leu Asn
 340 345 350
 Leu Phe Ser Leu Asp Pro Asp Ile Asp Thr Leu Lys Leu Gln Lys Lys
 355 360 365
 Asp Leu Leu Glu Pro Glu Ser Val Ile Lys Pro Phe Glu Glu Lys Ala
 370 375 380
 Ala Lys Arg Ile Met Ile Ile Cys Lys Ala Leu Asn Ser Asn Leu Gln
 385 390 395 400
 Gly Cys Val Thr Glu Asn Glu Asn Asp Pro Ile Thr Asn Ile Glu Pro
 405 410 415
 Phe Phe Val Ser Val Ala Leu Tyr Asp Leu Arg Asp Ser Arg Lys Ile
 420 425 430
 Ser Ala Asp Phe His Val Asp Leu Asn His Ala Ala Val Arg Gln Met
 435 440 445
 Leu Leu Gly Ala Ser Val Ala Leu Glu Asn Gly Asn Ile Asp Thr Ile
 450 455 460
 Thr Pro Arg Gln Ser Glu Glu Pro His Ile Lys Gly Leu Pro Glu Glu
 465 470 475 480
 Trp Leu Lys Phe Pro Lys Gln Ala Val Phe Ser Val Ser Asn Pro His
 485 490 495
 Ser Glu Ile Val Leu Val Ala Lys Ile Glu Lys Val Leu Met Gly Asn
 500 505 510
 Ile Ala Ser Gly Ala Glu Pro Tyr Ile Lys Asn Pro Asp Ser Asn Lys
 515 520 525
 Tyr Ala Gln Lys Ile Leu Lys Ser Asn Arg Gln Phe Cys Ser Lys Leu
 530 535 540
 Gly Lys Tyr Arg Arg Ala Phe Ala Trp Ala Val Arg Ser Val Phe Lys
 545 550 555 560

Asp Asn Gln Gly Asn Val Asp Arg Asp Ser Arg Phe Ser Pro Leu Phe
 565 570 575
 Arg Gln Glu Ser Ser Lys Ile Ser Thr Glu Asp Leu Val Lys Leu Val
 580 585 590
 Ser Asp Tyr Arg Arg Ala Asp Arg Ile Ser Lys Met Gln Thr Ile Pro
 595 600 605
 Gly Ser Leu Asp Ile Ala Val Asp Asn Val Pro Leu Glu His Pro Asn
 610 615 620
 Cys Val Thr Ser Ser Phe Ile Pro Val Lys Pro Phe Asn Met Met Ala
 625 630 635 640
 Gln Thr Glu Pro Thr Val Glu Val Glu Phe Val Tyr Asp Ser Thr
 645 650 655
 Lys Tyr Cys Arg Pro Tyr Arg Val Tyr Lys Asn Gln Ile Tyr Ile Tyr
 660 665 670
 Pro Lys His Leu Lys Tyr Asp Ser Gln Lys Cys Phe Asn Lys Ala Arg
 675 680 685
 Asn Ile Thr Val Cys Ile Glu Phe Lys Asn Ser Asp Glu Glu Ser Ala
 690 695 700
 Lys Pro Leu Lys Cys Ile Tyr Gly Lys Pro Glu Gly Pro Leu Phe Thr
 705 710 715 720
 Ser Ala Ala Tyr Thr Ala Val Leu His His Ser Gln Asn Pro Asp Phe
 725 730 735
 Ser Asp Glu Val Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His
 740 745 750
 His Ile Leu Phe Ser Phe Tyr His Val Thr Cys Asp Ile Asn Ala Lys
 755 760 765
 Ala Asn Ala Lys Lys Glu Ala Leu Glu Thr Ser Val Gly Tyr Ala
 770 775 780
 Trp Leu Pro Leu Met Lys His Asp Gln Ile Ala Ser Gln Glu Tyr Asn
 785 790 795 800
 Ile Pro Ile Ala Thr Ser Leu Pro Pro Asn Tyr Leu Ser Phe Gln Asp
 805 810 815
 Ser Ala Ser Gly Lys His Gly Gly Ser Asp Ile Lys Trp Val Asp Gly
 820 825 830
 Gly Lys Pro Leu Phe Lys Val Ser Thr Phe Val Val Ser Thr Val Asn
 835 840 845
 Thr Gln Asp Pro His Val Asn Ala Phe Phe Gln Glu Cys Gln Lys Arg
 850 855 860
 Glu Lys Asp Met Ser Gln Ser Pro Thr Ser Asn Phe Ile Arg Ser Cys
 865 870 875 880

Lys Asn Leu Leu Asn Val Glu Lys Ile His Ala Ile Met Ser Phe Leu
 885 890 895

 Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val Gln Asn Glu Glu
 900 905 910

 Asp Glu Ile Thr Thr Val Thr Arg Val Leu Pro Asp Ile Val Ala
 915 920 925

 Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln Ser Tyr Ile Lys
 930 935 940

 Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro Val His Glu Asp
 945 950 955 960

 Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn Asp Ser Pro Thr
 965 970 975

 Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe Ala Ile Ile Leu
 980 985 990

 Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys Ile Gln Leu Pro
 995 1000 1005

 Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu Leu Asp Asn Leu
 1010 1015 1020

 Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr Lys Asp Ala Leu
 1025 1030 1035 1040

 Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg Phe Leu Lys Arg
 1045 1050 1055

 Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys Met Val Asn Asn
 1060 1065 1070

 Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr Leu Cys Gln Tyr
 1075 1080 1085

 Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu His Phe Ile Pro
 1090 1095 1100

 Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp Pro Leu Thr Pro
 1105 1110 1115 1120

 Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met Pro Glu Tyr Ser
 1125 1130 1135

 Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile Gly Ile Leu Leu
 1140 1145 1150

 Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp Val Arg His Leu
 1155 1160 1165

 Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp
 1170 1175 1180

 Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met
 1185 1190 1195 1200

Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys
 1205 1210 1215
 Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp
 1220 1225 1230
 Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His
 1235 1240 1245
 Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val Leu Asn Ser Ile
 1250 1255 1260
 Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser
 1265 1270 1275 1280
 Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser Thr Asn Glu Lys
 1285 1290 1295
 Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala
 1300 1305 1310
 Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp Gln Ala Glu Thr
 1315 1320 1325
 Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr
 1330 1335 1340
 Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser Pro Glu Val Ser
 1345 1350 1355 1360
 Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn Phe Arg Tyr Leu
 1365 1370 1375
 Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val
 1380 1385 1390
 Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys
 1395 1400 1405
 Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His
 1410 1415 1420
 Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly
 1425 1430 1435 1440
 Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr
 1445 1450 1455
 Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr
 1460 1465 1470
 Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val
 1475 1480 1485
 Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys
 1490 1495 1500
 Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr Met Leu Phe Phe
 1505 1510 1515 1520

Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu
1525 1530 1535

Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe Gln Gly Pro Ala
1540 1545 1550

Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys Cys Cys Asn His
1555 1560 1565

Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu Leu Tyr Leu Phe
1570 1575 1580

Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser
1585 1590 1595 1600

His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile Ala Asp Ala Gly
1605 1610 1615

Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile Thr Asn Asn Phe
1620 1625 1630

Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val
1635 1640 1645

Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
1650 1655 1660

Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
1665 1670 1675 1680

Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu Arg Arg Thr Trp
1685 1690 1695

Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu
1700 1705 1710

Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu
1715 1720 1725

Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu
1730 1735 1740

Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr
1745 1750 1755 1760

Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser
1765 1770 1775

Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly
1780 1785 1790

Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr
1795 1800 1805

Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala
1810 1815 1820

Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe
1825 1830 1835 1840

Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys
1845 1850 1855

Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr
1860 1865 1870

Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Gly Lys
1875 1880 1885

Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser
1890 1895 1900

Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val
1905 1910 1915 1920

Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro
1925 1930 1935

Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu
1940 1945 1950

Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile
1955 1960 1965

Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His
1970 1975 1980

Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser
1985 1990 1995 2000

His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser
2005 2010 2015

Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg
2020 2025 2030

Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met
2035 2040 2045

Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn
2050 2055 2060

Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala
2065 2070 2075 2080

Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg
2085 2090 2095

Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu
2100 2105 2110

Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr
2115 2120 2125

Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr
2130 2135 2140

Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg
2145 2150 2155 2160

Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val Ser Ile Ser Ser
2165 2170 2175

Ser Ala Glu Val
2180

<210> 105

<400> 105

000

<210> 106

<400> 106

000

<210> 107

<400> 107

000

<210> 108

<400> 108

000

<210> 109

<400> 109

000

<210> 110

<400> 110

000

<210> 111

<400> 111

000

<210> 112

<400> 112

000

<210> 113

<400> 113

000

<210> 114

<400> 114

000

<210> 115

<400> 115

000

<210> 116

<400> 116

000

<210> 117

<400> 117

000

<210> 118

<400> 118

000

<210> 119

<400> 119

000

<210> 120

<400> 120

000

<210> 121

<400> 121

000

<210> 122

<400> 122

000

<210> 123

<400> 123

000

<210> 124

<400> 124

000

<210> 125

<400> 125

000

<210> 126

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus furin cleavage sequence

<400> 126

Arg Lys Gln Arg

1

<210> 127

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:furin cleavage sequence homolog in human CLASP-3

<400> 127

Arg Lys Ser Arg

1

<210> 128

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CLASP-3 immunoreceptor tyrosine-based activation motif (ITAM) motif 1

<220>

<221> MOD_RES

<222> (1)..(11)

<223> Xaa = any amino acid

<400> 128

Tyr Xaa Xaa Val Xaa Xaa Xaa Tyr Xaa Xaa Leu

1 5 10

<210> 129
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CLASP-3
immunoreceptor tyrosine-based activation motif
(ITAM) motif 2

<220>
<221> MOD_RES
<222> (1)..(10)
<223> Xaa = any amino acid

<400> 129
Tyr Xaa Xaa Val Xaa Xaa Tyr Xaa Xaa Lys
1 5 10

<210> 130
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CLASP-3
immunoreceptor tyrosine-based activation motif
(ITAM) motif 3

<220>
<221> MOD_RES
<222> (1)..(13)
<223> Xaa = any amino acid

<400> 130
Tyr Xaa Xaa Ile Xaa Xaa Xaa Xaa Tyr Xaa Xaa Thr
1 5 10

<210> 131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:highly
conserved non-tyrosine containing region from
motif E

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = conservative amino acid substitution, Xaa =
Ile or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = any amino acid

```
<220>
<221> MOD_RES
<222> (7)
<223> Xaa = conservative amino acid substitution, Xaa =
      Asp, Glu or Gln

<220>
<221> MOD_RES
<222> (8)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (9)
<223> Xaa = conservative amino acid substitution, Xaa =
      Met, Ile, Leu or Val

<400> 131
Pro Xaa Glu Xaa Ala Ile Xaa Xaa Xaa
    1           5

<210> 132
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:highly
      conserved non-tyrosine containing region from
      motif F

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Met or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = conservative amino acid substitution, Xaa =
      Gln or Asn

<220>
<221> MOD_RES
<222> (8)
<223> Xaa = any amino acid
```

```

<220>
<221> MOD_RES
<222> (9)
<223> Xaa = Val or Ile

<220>
<221> MOD_RES
<222> (10)..(12)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (15)
<223> Xaa = any amino acid

<400> 132
Leu Xaa Xaa Xaa Leu Xaa Gly Xaa Xaa Xaa Xaa Xaa Val Asn Xaa Gly
    1           5           10          15

<210> 133
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense oligo
      1

<400> 133
ctattactaa ggcttcgaga acgattta                                28

<210> 134
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense oligo
      2

<400> 134
ctggaaaacg acttttcctt ggagcctcaa g                                31

<210> 135
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense oligo
      3

<400> 135
gtgctgctga gtggactaga cactgtgcag c                                31

```

<400> 140
gacc cattag gaggtctac 19

<210> 141
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense primer HC4AS3'

<400> 141
cgggatccat tgtcaccgta catctgc 27

<210> 142
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sense primer hC1S5'

<400> 142
tatgtctcag tcacctacct g 21

<210> 143
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense primer HC1AS3'Kpn

<400> 143
cttggtagcca cttcaggact agatgagatg 30

<210> 144
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sense primer C1S7

<400> 144
tcaagaccag ggcattgcaag 20

<210> 145
<211> 29
<212> DNA
<213> Artificial Sequence

Jan
A/3

<220>
<223> Description of Artificial Sequence:HC3RACE5 primer
used for human CLASP-3 5' RACE

<400> 145
aaaaacatct tgccaaggat aagtgatag

29

<210> 146
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HC3RACE6 primer
used for human CLASP-3 5' RACE

<400> 146
attgctgatc ttgccagggt agtaatgg

28

<210> 147
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HC3RACE7 primer
used for human CLASP-3 5' RACE

<400> 147
tgccggaaac tctaagattt ctctggtag

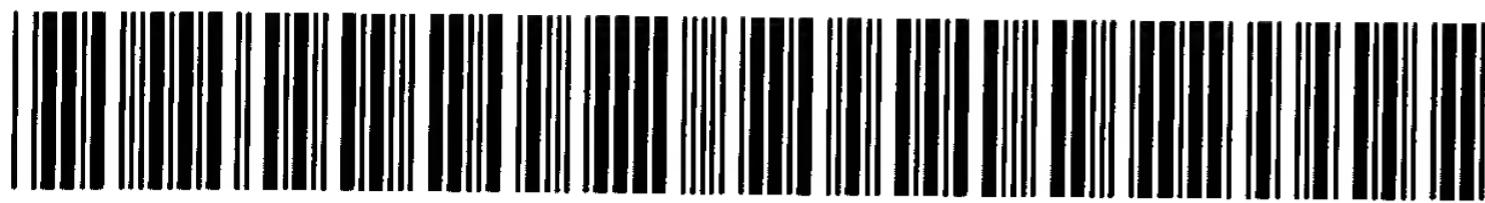
29

<210> 148
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HC3RACE8 primer
used for human CLASP-3 5' RACE

<400> 148
ttcacttcaa gcacgtccgg agttaggc

28



Creation date: 09-29-2003

Indexing Officer: AWILSON2 - ANDREA WILSON

Team: OIPEBackFileIndexing

Dossier: 09737246

Legal Date: 10-04-2001

No.	Doccode	Number of pages
1	CRFL	7

Total number of pages: 7

Remarks:

Order of re-scan issued on